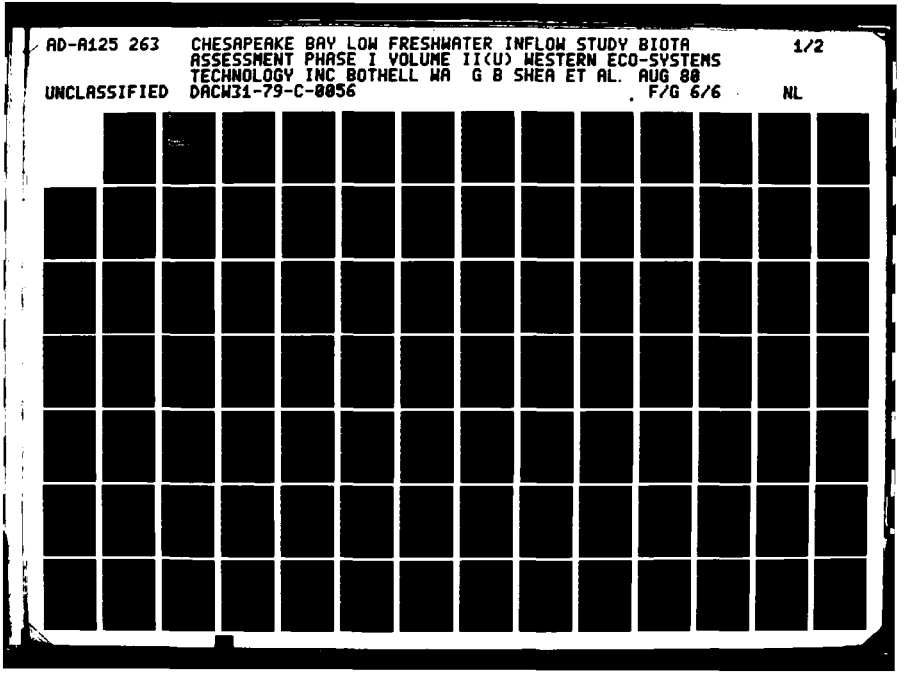
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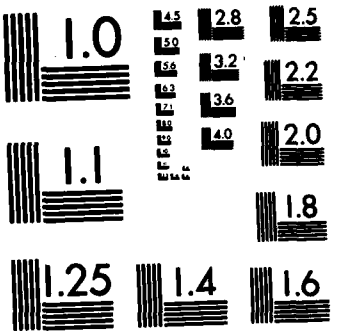

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Chesapeake Bay Low Freshwater Inflow Study
Biota Assessment

Phase I
Volume II

Prepared for
U.S. Army Engineer District Baltimore
by Western Eco-Systems Technology, Inc.

August 1980

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Phase I of this report consists of a 2-volume report plus one appendix containing species tolerance and habitat information.
Phase II consists of a one-volume report and a supplementary MAP FOLIO.

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20. ABSTRACT (Continue on reverse side if necessary and identify by block number)

An assessment of the effects of low freshwater inflow conditions on the biota of Chesapeake Bay was conducted through use of data output from the U.S. Army Corps of Engineers' Chesapeake Bay Hydraulic Model. Phase I of the biota assessment focussed on methodology development and establishment of a baseline for determination of freshwater inflow-induced change. Physical and chemical information, along with salinity tolerance and other habitat related information was collected for a group of over 50 study organisms.
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20. ABSTRACT (continued)

In Phase II of the assessment, four sets of hydraulic model test conditions (scenarios) were used which simulated effects of drought and effects of future consumptive water use as deviations from present average flow conditions. Changes in habitat for the selected study organisms were predicted and mapped based on salinity and other variables. Changes in habitat, which were used to delineate the amount of impact from reduced freshwater inflow, were found to include increases and decreases depending on the species, its lifecycle, tolerances, and interactions with other organisms. The magnitude of habitat change was found to generally increase as salinity changes increased.

CHESAPEAKE BAY LOW FLOW STUDY:

BIOTA ASSESSMENT

PHASE I: FINAL REPORT

VOLUME II

August 1980

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Submitted to:

U.S. Army Corps of Engineers
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The American University

Virginia Institute of Marine Science

Virginia Marine Resources Commission

Virginia Fish and Game

National Marine Fisheries Service

- Resource Statistics Division
- Oxford Laboratory

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V. BIOTA

This chapter is the second of three chapters which discuss various aspects of the inpact assessment methodologies developed in Phase I of the Biota Assessment. While the previous chapter focused on defining baseline, this chapter discusses the selection of study species and the distributional mapping of those study species. Chapter VI, which follows, works through the development of conceptual and mathematical ecological models.

One of the first steps in selection of study species was to delineate the various organisms by major functional groups. These have already been discussed in Chapter III and elsewhere, but are defined here in terms of their relationship to selection of study species.

A. MAJOR GROUPS

To simplify our ecosystem analysis and study species selection, we have grouped the living components of the Chesapeake Bay ecosystem into seven cagegories which reflect both function and habitat as follows.

Phytoplankton: These are microscopic, unusally single-celled plants which represent several divisions of algae. Functionally, the group comprises both net- and nanno-plankton, the latter being species less than 10 μm diameter (Van Valkenburg and Flemer 1974). Phytoplankton are pelagic, and are moved about by actions of currents and tide. Some workers further distinguish ultra-plankton, species less than 2 to 3 μm. This category would include most planktonic bacteria, which are heterotrophs and, as a group, not well-known in the Bay.

Submerged Aquatic Vegetation: These are plants - usually rooted - which live submerged below the water's surface. Submerged aquatics in Chesapeake Bay are chiefly angiosperms (seed plants), although some species (e.g. Nitella) are macroalgae.

Emergent Aquatic Vegetation: These are plants which grow partially submerged, regularly or occasionally flooded, or in

wet soils. They make up the bulk of vegetation in marshes and other wetlands.

Zooplankton: These are usually small, sometime microscopic, animals from several phyla. The group is composed of holoplankton, species which are planktonic throughout life, and meroplankton, species which spend only part of their life cycle in the plankton.

Benthos: The benthos is comprised of organisms, mainly invertebrates, which live associated with the substrate. These may be epifauna - species which live attached on or above the bottom - or infauna, species which burrow into the substrate. Some species, such as crabs, are benthic oriented, but are motile or vagile, capable of considerable swimming. Other species are benthic only at some stage of their life cycle, such as the sea nettle (Chrysaora quinquecirrha). The benthos is often divided into macro - (greater than 0.5 mm), meio - (0.5 - 0.1 mm), and micro - benthos (less than 0.1 mm) (Coull 1973). Of these, only the macro-benthos is well-known in Chesapeake Bay (Lippson et al. 1979).

Fish: Fish make up the bulk of the Chesapeake Bay nekton-species, which exhibit well-developed powers of movement. Dermersal fishes are those, such as spot (Lieostomus xanthurus) which are associated with the bottom and feed chiefly on benthic organisms. Pelagic species feed in the water column, chiefly on fish and macroinvertebrates.

Wildlife (Amphibians, Reptiles, Birds, and Mammals): Numerous waterfowland shorebirds, and some water-oriented amphibians, reptiles, and mammals use the estuary and adjacent wetlands for food, shelter, and breeding areas. The dependence on the estuary varies from species to species. Many of the birds are migratory and use the estuarine resources seasonally.

B. DISTRIBUTION OF ESTUARINE ORGANISMS

It is generally acknowledged that the distributions of estuarine organisms do not have the sharp boundaries implied by the Venice

System (Wolff 1973, Boesch 1977). Rather, each species population itself exhibits a continuum or cline along the estuarine complex-gradient; the point of maximum abundance reflects both innate physiological tolerances and effects of biotic and abiotic features of the environment (Whittaker 1970). Apparent discontinuities may result from substrate changes, effects of competition, or the overlapping of similar distributions along the estuarine gradient (Boesch 1971, Wolff 1973).

Nevertheless, there is evidence that some correlation exists between the Venice System boundaries and estuarine biotic zonation. Dahl (1956) reviewed numerous studies from brackish environments and identified three zones of more rapid biotic change, at 0.1 - 0.5‰ , 5.0 - 8.0‰ , and 15.0 - 20.0‰. Khlebovich (1969) characterizes the salinity range between 5.0 - 8.0‰ as the "critical salinity"; below this range, hyperosmotic regulation is required to prevent internal salinity from dropping below 4.0 - 5.0 ‰ (at which point serious tissue damage occurs). Kinne (1963, 1964) divides animals into four groups based on their osmoregulatory abilities, although there is variation within each group. These groups are:

- stenohaline osmoconformers, with little or no capacity for regulation,
- euryhaline osmoregulators, which can regulate in water of reduced salinity, but not fresh water,
- holeuryhaline osmoregulators, which can regulate from fresh to full oceanic salinities , and
- oligohaline osmoregulators, which can regulate only in fresh water and very low salinities, and maintain blood hyperosmotic to the external medium.

The estuarine biota is thus composed of organisms which show varying amount of adaption to conditions within that environment.

Day (1951, 1967) first recognized five major components in South African estuaries: fresh water, true estuarine, euryhaline marine, stenohaline marine, and migratory. Carriker (1967) relates these to the Venice System boundaries, and characterized each group by general salinity tolerances, origin,

and reproductive requirements. Boesch (1971, 1977) further refines this classification and recognizes the following major groups:

Stenohaline Marine: These organisms are characteristic of euhaline environments, but occasionally penetrate the estuary to 25.0 ‰. Within Chesapeake Bay they are restricted to the polyhaline zone. Example: the cladoceran Evadne tergistina (Bryan 1977).

Euryhaline Marine: The organisms extend from the euhaline zone into the estuary, sometimes to relatively low salinities (15.0ppt). This group comprises the larges part of the estuarine biota in the polyhaline zone. Some species depend on recruitment from the marine environment, but many have viable reproducing populations within the estuary. Example: the venerid clam Mercenaria Mercenaria.

Euryhaline Opportunists: These are species which are found from the euhaline zone (often) to the oligohaline zone. However, they are generally most numerous in the low polyhaline and mesohaline reaches of the estuary. Their reproductive strategy allows them to colonize rapidly disturbed or stressed habitats, as well as salinity regimes where less eurytopic species are a competive disadvantage (Carriker 1967, Boesch 1971, 1977). Example: the polychaete Heteromastus filiformis.

True Estuarine or Estuarine Endemics: These species are restricted to the estuary, either by physiological limitation at some part of their life cycle or by competition with marine species in offshore environments (Kinne 1966, Day 1967, Jefferies 1967, Diaz 1977). Some may be restricted to the estuary, however, by substrate or circulation requirements (Day 1967, Boesch 1971). In general, they are dominant members of the biota below 15.0ppt. Example: the mactrid clam Rangia cuneata.

Tidal Fresh Water and Oligohaline: These species are derived from fresh water forms, but are able to tolerate varying amounts of salt. Most are restricted to salinities

below 0.1 ‰, but some persist to 5.0‰ or higher (Carriker 1967, Diaz 1977). In general, the biota of the tidal fresh water and oligohaline zones consists of a mixture of a few eurytopic fresh water species and estuarine endemics (Diaz 1977). Example: the tubificid worm Limnodrilus hoffmeisteri.

The first four of these categories of organisms are of marine origin, and have adapted to the estuary to varying degrees.

Boesch (1977) has developed a general model of estuarine zonation, based on distribution of benthic invertebrates along the Chesapeake bay - York River gradient (see Figure III-14). He found faunal changes to be gradual, with zones of somewhat accelerated change in the 3.0 - 8.0‰ and the 15.0 - 20.0‰ range. There is a gradual decrease in species richness from the polyhaline to the oligohaline zone. Diaz (1977) found the lowest diversity of benthic macro-invertebrates in the oligohaline and tidal freshwater zones of the James River, with an increase in diversity in non-tidal freshwater areas. The oligohaline/tidal freshwater zones were high energy environments, which were turbid, with a low diversity of benthic habitats.

This general model of distribution does not hold as well for some other groups. Planktonic organisms can be carried into areas outside their normal salinity range by actions of currents and tides. Typically, "fresh-water" phyto- and zooplankton are found throughout the oligohaline zone, and often carried into the low mesohaline by normal riverflow (Goodwyn 1970). Species typically found in euhaline or polyhaline environments may be carried into the estuary in the inflowing deep layers, later being admixed into upper layers of lower salinity zones (Burrell 1972). Fish are able to move with relative freedom within their range of physiological tolerances. Euryhaline marine species such as menhaden will be found much further upstream than is shown in Figure III-14,whereas estuarine endemics

such as killifish are found further downstream. Larval fishes, however, ususally have more restricted ranges due to their limited osmoregulatory abilities (Polgar et al.1976).

It is a generality that species richness and diversity is lowest in the oligohaline zone, although this is not equally true for all groups. Over 540 species of phytoplankton were recorded from a non-tidal freshwater site on the Potomac (ANSP 1972), while only 160 taxa were recorded from the tidal freshwater/oligohaline zone by Dahlberg (1973). Even fewer species (around 80) were found at Maryland Point on the Potomac, a variable oligohaline/low mesohaline area in the estuarine transition zone (Mountford 1971). While Morse (1947) identified over 200 from the mesohaline region at the mouth of the Patuxent, total species number obtained from several surveys in the Bay's polyhaline zone add up to over 205 taxa (Patten et al. 1963, Marshall 1967, Mackiernan 1968).

The number of zooplankton species is generally high in freshwater areas, in part due to the diversity of rotifers and cladocerans in this environment (Dahlberg et al. 1973). At Douglas Point, 116 species were recorded, of which 33 were rotifers and 25 cladocerans. Similarly, much of the increased species richness of macroinvertebrates in freshwater environments is due to the high proportion of insect larvae; at the non-tidal Dickerson site, 387 out of 452 species were insects, while 38 species out of 76 were insects at Douglas Point (Dahlberg et al. 1973). In the oligohaline zone the majority of these salt intolerant forms dissappear.

Submerged and emergent vegetation have their highest diversity and species richness in the lower salinity areas, although for marsh species the period and extent of tidal inundation is more important than salinity in determining distribution (Boon et al. 1977, Orth et al. 1979). There are relatively few submerged higher plant species found in polyhaline and

euryhaline environments; in Chesapeake Bay only Zostera marina and Ruppia maritima occupy this zone (Orth et al. 1979).

It is apparent that the observed biotic zonation of the estuary reflects changes in importance of the major components along the ecocline. A generality which can be made is that the organisms of marine origin are limited up-estuary by salinity constraints, and down-estuary by biological interactions, although in some cases salinity again becomes a limiting factor (Larsen 1974, Boesch 1977, Diaz 1977, Heinle et al. 1978).

Estuarine endemics and euryhaline species often show greater range of salinity tolerance in the laboratory than is realized in the environment (Cain 1974, Castagna and Chanley 1973). They may be restricted to lower salinities by predation (Kinne 1966, Larsen 1974) or by narrow salinity tolerances of a particular life stage (Cain 1972, Tagatz 1968). Such estuarine species need to have mechanisms for retention of their larvae and juveniles within the estuary. Some brood their young, or have non-planktonic larval stages (eg. the oyster drill Urosalpinx cinerea). This, however, reduces their ability to colonize new habitat or former habitat from which they have been eliminated (D. Haven, personal communication). Many species with planktonic larvae have evolved behavioral mechanisms which take advantage of estuarine circulation to enter or remain within the estuary, eg. oyster larvae, blue crab megalopes, larval fish (Harrison et al. 1967, Wood and Hargis 1971, Sandifer 1973, 1975).

C. INITIAL STUDY SPECIES SELECTION

The Chesapeake Bay Low Flow Study requires that "approximately fifty" study species will be used to assess the biotic effects of low fresh water inflows. Selection of these study species, and justification of their choice, is an extensive task. It is estimated that over 2650 species of plants and animals live within

the Chesapeake Bay (McErlean et al. 1972). These include commercially and recreationally important forms, as well as numerous species which represent major links in the estuarine trophic structure.

In order to assess the effects of perturbations on the tidal ecosystem, study species should represent taxa and functional groups from the major Bay habitats, salinity zones, and biotic subcomponents. Swartz (1972) emphasized that selection of test organisms should be based on their relative vulnerability to change and stress, ecological significance, distribution within the estuary, phylogenetic representation, and economic significance. To this should be added the practical consideration of data availability for each species.

With Swartz's criteria in mind, a preliminary list of 167 potential study species was generated and circulated at the November 1979 seminar (see Chapter II). This was based on a variety of sources, including the following published list of major Chesapeake Bay species:

- Chesapeake Bay Existing Conditions Report (USACE 1973): A list of 110 species recommended for bioassay or condition indices, in order to assess effects of environmental stress (Swartz 1972).
- Chesapeake Bay Future Conditions Report (USACE 1977): A list of 126 important species and genera, based on a survey of Bay researchers. Species were included on this list on the basis of 15 criteria, including importance to trophic structure, and distribution. An attempt was made to include species representing as many Chesapeake Bay habitats as possible.
- Maryland Department of Natural Resources list of 44 representative species from tidal and non-tidal waters. These species are to be used in studies assessing impact of discharges into natural waters.

In addition, numerous reports, papers, and data sets were consulted to identify major species, and their general distribution in regard to salinity. The following were major sources used to generate the initial study species list.

Phytoplankton: Patten et al. 1965; Marshall 1966, 1[illegible]; Mackiernan 1968; Mulford 1972; Dahlberg et al. 1973; Van Valkenberg and Flemer 1974; Seliger et al. 1975; Lear and Smith 1976; Mountford 1977; Van Valkenburg et al. 1978.

Submerged Aquatic Vegetation: Orth 1975, Stevenson and Confer 1978; Anderson 1979 unpublished data; Orth et al 1979; Munro 1979; Migratory Bird Habitat Reseach Laboratory, unpublished data.

Emergent Aquatic Vegetation: Maryland Wetlands Survey, DNR, 1967 - 1968; Keefe 1973; Metzgar 1973; Virginia State Wetlands Survey Series, VIMS, 1973 - 1978; Boon et al. 1977.

Zooplankton: Heinle 1966, 1969; Herman et al. 1968; Bosch and Taylor 1968, 1973; Goodwyn 1970; Burrell & Van Engle 1976; Dahlberg et al. 1973; Heinle et al. 1975; Sage et al. 1976; Bryan 1977; Grant 1977; Sage and Olsen 1977; Jacobs 1978; Grant and Olney 1979; Lippson et al. 1979.

Benthic Organisms: Corey 1967; Pfitzenmeyer 1961, 1970, 1973, 1975, 1976; Boesch 1971, 1972, 1973, 1977; Wass et al. 1972; Hamilton and LaPlante 1972; Davies 1972; Orth 1973; Larsen 1974; Diaz 1977; Mountford et al 1977; Virnstein 1977, 1979; Haven et al. 1977, 1979; Lippson et al. 1979; Reinharz, Bricker & O'Connell 1979; Cory and Dresler 1980, unpublished data.

Fish: Hildebrand and Schroeder 1928; Smith et al.1966; Ritchie 1970; Douglas and Stroud 1971; National Marine Fisheries Service Fishery Statistics of the U.S. 1976 - 1978; Scott and Boone 1973; Lippson and Moran 1974; W.R. Carter, unpublished data; NMFS Current Fishery Statistics 1975 - 1978.

Birds and Mammals: Dozier 1947; Stewart 1962; Willner et al. 1975; Perry and Uhler 1976; Maryland Dept. of Natural Resources, Midwinter Waterfowl Surveys 1975 - 1980; Virginia Fish and Game, Midwinter Waterfowl Surveys 1975 - 1980; Rawls, unpublished M.S.

Eight basic selection criteria were used to choose species for the original list. These were:

Sensitivity to Salinity: Salinity tolerances for candidate species (see App. B) were evaluated from several sources: laboratory studies; field studies, and extrapolation from field collection data. Although the majority of estuarine organisms tend to be rather euryhaline, many exhibit greater stenotopy at certain stages of their life cycle; eg. Rangia cuneata, the larvae of which require salinities between 2 - 10 ‰ to survive (Cain 1974, Hopkins et al. 1973). Laboratory studies commonly demonstrate a wider range of salinity tolerance than the species exhibits under field conditions (Castagna and Chanley 1973). This may reflect interaction of salinity with some other factor such as temperature or substrate, range restriction due to predation or competition, or a stenotopic life stage (Kinne 1966, Van Engel 1958, Boesch 1977).

Sensitivity to Other Factors: Chief among these would be factors which themselves might be affected by salinity or low fresh water inflows:

Circulation: A partially mixed, moderately stratified estuary such as Chesapeake Bay is characterized by a net seaward flow of lower salinity upper layers and a net upstream flow of higher salinity deep water (Pritard 1956, 1967). In general, the outflow at the surface is the driving force for the rate of inflow of higher salinity bottom water (Pritchard 1967, Tyler and Seliger 1978). Many organisms use the upstream movement of

water at depth to transport themselves into and maintain themselves within the estuary (Haven 1957, Harrison et al. 1967, Wood and Hargis 1971, Sandifer 1973, 1975). Reduced freshwater inflow could alter the rate of transport, and allow breakdown of density stratification, particularly in the tributary rivers (Schubel 1972). This could have effects beyond simple salinity tolerances, if important commercial species such as blue crabs, croaker and spot are prevented from reaching their upstream nursery areas, or oysters their upstream beds.

Temperature: The synergistic effects of temperature and salinity have been described by Kinne (1963, 1964) and others. Temperature stress can narrow the salinity tolerance zone for many organisms, and vice versa. For example, in lower salinities, the copepod Arcartia tonsa has a competitive advantage over the congeneric A. clausi at temperatures from 11 to 18° C, as it is less affected by the salinity stress (Jeffries 1962). Chesapeake Bay represents the maximum northward range extension of several southern species such as Rangia cuneata, and the southernmost extension of others such as Mya arenaria. Adverse salinities during cold or warm periods, respectively, could have a more severe effect than that produced by salinity alone.

Food: Some species, themselves euryhaline, are dependent on a more stenotopic food source. For example, the redhead (Aythya americana) feeds extensively on Potamogeton spp. (pondweeds), plants restricted to oligohaline and low mesohaline areas (Stewart 1962, Stevenson and Confer 1978).

Substrate: Although most benthic organisms show a certain eurytopy as to substrate, sediment preferences do exist (Kinner et al. 1974, Maurer et al. 1978). For

example, sandy substrates are most numerous in the lower Bay, particularly near the Bay mouth, restriction of certain species to this section of the estuary is less a reflection of their stenohalinity as it is of their psammophilic nature (Boesch 1971, 1977). Changes in fresh water inflow might not only alter the areas of certain substrate within a particular salinity zone, but could change sedimentation rates and sediment types in parts of the Bay and its tributaries (Hart and Fuller 1972, Schubel 1972, Sharaf el Din 1977, Snedaker et al. 1977).

Affected by Biological Interactions: As discussed earlier, these interactions include predation, parasitism, competition, and disease. Many estuarine endemics and euryhaline opportunists find the estuary a refuge from predation and competition (Kinne 1966, Hodgkin and Rippingdale 1971, Boesch 1977). There are numerous examples of euryhaline species having restricted ranges due to incresed predation in higher salinities. For example, the oyster Crassostrea virginica is predated in salinities above 15 ‰ by the oyster drill Urosalpinx cinerea, and suffers heavy mortalities in salinities above about 12 ‰ due to the protozoan parasites Minchinia nelsoni (MSX) and Perkinsus marinus ("dermo") (Carriker 1955, Gunter 1955, Andrews 1967, Sprague et al. 1969, Haven et al. 1978). Although predation seems to be the most important factor, at least for benthic forms (Virnstein 1977, 1979), Evidence exists that competitive exclusion may restrict ranges of some species, eg. Macoma balthica versus M. tenta (Boesch 1971).

Represent Key Trophic Links: Certain species, because of their numbers, productivity, or distribution, represent major links in the Chesapeake Bay food web. Results of caging experiments, stomach analyses, and laboratory feeding studies have been used to identify major food items, food selectivity, ingestion rates and vulnerability to predation for candidate study species (Heinle 1966, 1974; Burrell 1972; Perry and Uhler 1976; Homer

and Boyton 1978; Holland et al. 1979; Rawls, unpublished M.S.; and others). Some abundant species are numerous because they have evolved means to avoid predation, and are thus not key trophic links (Virnstein 1977, 1979). However they may be important for other reasons, such as substrate modification or nutrient cycling.

Perform Key Ecosystem Processes: These functions might include nutrient recycling, substrate modification or habitat production. Benthic organisms (particularly by the meio- and microcomponents), as well as zooplankton and fish, excrete nitrogenous and phosphorous containing compounds; these can be utilized by phytoplankton and rooted aquatics for primary production (Coull 1973, Hale 1976, Durbin 1976, Taft and Taylor 1976, Kremer 1977, McCarthy et al. 1977). Modification of substrate can be positive or negative. Certainspecies, particularly polychaetes, produce tubes which bind loose sediments and stabilize the bottom, allowing colonization by other organisms (Kinner and Maurer 1978, Virnstein 1979). However, bioturbation by benthic infauna, as well as accumulation of fecal material can create a loose flocculant substrate inhibitory to many species(Rhoads and Young 1970, Levinton 1977). Prey-seeking behavior by fish and crabs can also disrupt the substrate, reducing numbers and diversity of species found (Orth 1975, Virnstein 1977, 1979).

Certain species so physically dominate their environment that they themselves constitute the habitat. In Chesapeake Bay, major examples are the oyster reef and its associates, and submerged aquatic vegetation beds. Density and diversity of species in these habitats are greater than in surrounding sand or mud bottoms, and productivity can be significantly higher (Marsh 1973, Orth 1973, Bahr 1974, Larsen 1974, and Penhale 1977). Many researchers consider these species associations to represent biocoenoses, with complex interactions between their biotic components (Wells 1961, Marsh 1973). However, Larsen

(1974) cautions that, at least in the case of the oyster community, few of the associated species are obligates; rather, the physical structure of the reef provides hard substrate for a number of epifaunal species, as well as shelter for a variety of infauna.

Commercially or Recreationally Important Species: Organisms which are harvested by man, or which provide non-consumptive recreation are the measure by which the public tends to gauge the "health and productivity" of the estuary. Most of these species (eg. sport fish, crabs, and waterfowl) are large and conspicuous; many feed fairly high on the trophic chain. Their continued abundance depends on the integrity of the trophic web supporting their populations.

Threatened and Endangered Species: A number of threatened and endangered species inhabit the Chesapeake Bay area (U.S. Fish and Wildlife Service 1979). Some of these are birds and mammals which are more or less water-oriented, and may depend on the estuary seasonally or for some aspect of their needs (food, shelter, etc.). Examples are: Bald Eagle (Haliaeetus leucocephalus), Delmarva Fox Squirrel (Sciurus niger cinereus). Others are fish or reptiles which have been known to enter the Chesapeake Bay, or which at one time were resident, Examples are: Shortnose Sturgeon (Acipenser brevirostrum), Maryland Darter (Etheostoma sellare) (U.S. Fish and Wildlife Service 1979).

Availability of Data: Some organisms are important based on the above criteria, but lack adequate biomass, distribution, tolerance, and trophic information to be useful study species. Only those that have been well studied in terms of distribution were included in the preliminary list.

D. INTERMEDIATE AND FINAL SPECIES SCREENING CRITERIA

1. Intermediate Screening

Reduction of the preliminary list of 167 species required two subsequent screening steps. Selection of the final study species proceeded as follows.

The original list, with some additions suggested by reviewers, was reevaluated using eight criteria listed below. To facilitate this intermediate screening, a series of charts was developed for consolidation of data from numerous sources. Information gathered on these species included:

1. Salinity range and tolerance, both in the field and from laboratory studies, for each potentially sensitive life stage. If the study was from an area other than Chesapeake Bay, this was noted.
2. Temperature tolerances, both from field and laboratory information. Of particular importance were lethal temperatures, and temperature ranges affecting periods of reproduction and growth.
3. Biomass and abundance information, from Chesapeake Bay and other areas. Seasonality, as it affected biomass, etc. was noted.
4. Physiological rates, including respiration, growth, and production (of plants). Variation in these rates as correlated with salinity or temperature were noted when available. Many of these rates were taken from studies conducted on candidate species in areas other than Chesapeake Bay.
5. Preferred substrates for species (when applicable).
6. Trophic relationships, including preferred food or prey, major predators, feeding rates and predation rates, both from Chesapeake Bay and from other areas.

Changes in rates due to salinity of temperature were noted, when available.

7. Competitors, disease predators, and other limiting biotic factors. Information from areas other than Chesapeake Bay was taken when the same species were involved (i.e. candidate species and its competitor or disease). Historical changes in distribution of important diseases or predators due to salinity changes were noted.

8. Other limiting factors of a physical nature, such as light, depth, turbidity, etc. were noted when the information was available.

The task of filling out these charts for each of the 167 candidate species provided a chance to evaluate the adequacy and scope of information for each. Gaps in the literature were so extensive that some organisms were immediately eliminated. Chiefly on the basis of availability of data, as well as apparent ecosystem importance, and sensitivity to a variety of factors, the initial list was reduced to a second list of 81 species and associations. Because of the nature of the available data, associations rather then species were used for phytoplankton and emergent aquatic vegetation. Year to year variability in dominance of individual phytoplankton species, but relative stability in the overall seasonal associations led to this decision in the case of phytoplankton. Difficulty in resolving differences in Maryland and Virginia wetlands surveys necessitated the use of recurrent plant associations rather than individual species.

In developing this intermediate list, an attempt was made to include representative organisms from the various Venice System zones, and from the major ecological groups (i.e., estuarine endemics, euryhaline marine, etc.).

2. Final Study Species Screening

Final reduction of the intermediate species list involved construction of a species screening matrix. The 81 species and associations were evaluated against eighteen weighted factors (Table V-1) species being ranked on a scale of 0 - 4 in each of these criteria. The ranking value and the weighted value were multiplied to give a score for each factor, and these summed for a final score for each species. Cutoff values were assigned to these scores, and species with scores above these levels became final study species (Table V-2). Cutoff values varied between functional groups (i.e. zooplankton,benthos) because all eighteen screening factors did not apply to every group.

Considerable discussion entered into the assigning of weighting values to the final screening criteria, and these values generated a predictable amount of comment from reviewers. Selective judgments had to be made in assigning weight to the screening factors, and in ranking each species against them. However, it is hoped that at least some of the bias inevitable in developing any list of "major species" has been avoided.

Screening criteria used were essentially those discussed in Section V-C. However, these were expanded into 18 major components. That is, the category "Performs Key Ecosystem Functions" was broken down into "Important to Nutrient Cycling', "Affects Water Quality", and "Modifies Habitat for Other Species". The greatest weight was given to factors which could be affected by low freshwater inflow (eg. salinity sensitivity, dependence on estuarine circulation) or which measured a species' importance to the ecosystem (trophic dominance, biomass, major predator, etc.). Also, by necessity, the availability of data needed for mapping assessment of known and potential habitat, and trophic information for ecosystem analysis were heavily weighted. Values for other criteria were assigned by comparing their relative importance with the heavily weighted factors discussed above.

TABLE V-1

FINAL SPECIES SCREENING CRITERIA

Eighteen screening factors used in species selection matrix, with weighting values for each.

Factor	Weighting Value
Sensitive to Salinity	4
Sensitive to Circulation Changes	3
Sensitive to Substrate	2
Important to Nutrient Cycling	2
Affects Water Quality	1
Major Biomass Contribution	3
Wide Distribution in Bay	1
Rare or Endangered Species	1
Trophic Importance	4
Specialized Food Requirements	3
Major Predator	3
Major Competitor	1
Economic or Social Importance	1
Opportunistic Colonizer	1
Modifies Habitat for Other Species	2
Distribution Data Available	4
Trophic Data Available	3
Sensitive Life Stages	2

TABLE V-2

Final Study Species List

PHYTOPLANKTON ASSOCIATIONS	
Winter/Spring Associations	*Cyclotella meneghiniana/Melosira granulata* tidal freshwater association
	Katodinium rotundatum/Skeletonema costatum oligohaline, low mesohaline association
	Asterionella japonica/Skeletonema costatum dominated mesohaline association
	Nitschia pungens atlantica/Skeletonema costatum/Chaetoceros spp. dominated polyhaline association
Summer/Fall Associations	*Anacystis/Microcystis* tidal freshwater association
	Gymnodinium spp./*Prorocentrum minimum* dominated oligohaline, low mesohaline associations
	Gymnodinium/Chaetoceros/Skeletonema dominated high mesohaline polyhaline associations

SUBMERGED AQUATIC VEGETATION	
Ceratophyllum dermersum	hornwort
Potamogeton	pondweeds
Ruppia maritima	widgeon grass
Zanichellia palustris	horned pondweed
Zostera marina	eelgrass

EMERGENT AQUATIC VEGETATION ASSOCIATIONS	
Tidal Freshwater Associations	
Spartina spp. dominant, brackish tidal marsh	
Juncus roemerianus dominant, brackish tidal marsh	

ZOOPLANKTON		
Ctenophora	*Mnemiopsis leidyi*	ctenophore
Cnidaria	*Chrysaora quinquecirrha*	sea nettle
Rotifera	*Brachionus calcyiflorus*	rotifer

TABLE V-2
(Cont.)

	ZOOPLANKTON Cont.	
Crustacea	*Acartia clausi*	copepod
	Acartia tonsa	"
	Eurytemora affinis	"
	Scottolana canadensis	"
	Bosmina longirostris	cladoceran
	Evadne tergestina	"
	Podon polyphemoides	"
	BENTHOS	
Annelida	*Limnodrilus hoffmeisteri*	oligochaete worm
	Heteromastus filiformis	polychaete worm
	Pectinaria gouldii	"
	Scolecolepides virdis	"
	Streblospio benedicti	"
Mollusca	*Urosalpinx cinerea*	oyster drill
	Crassostrea virginica	oyster
	Macoma balthica	Baltic macoma
	Mercenaria mercenaria	hard clam
	Mulinia lateralis	coot clam
	Mya arenaria	soft clam
	Rangia cuneata	brackish clam
Crustacea	*Ampelisca abdita*	amphipod
	Balanus improvisus	barnacle
	Callinectes sapidus	blue crab
	Cyathura polita	isopod
	Gammarus daiberi	amphipod
	Leptocheirus plumulosus	"
	Palaemonetes pugio	grass shrimp

TABLE V-2
(Cont.)

FISH	
Alosa sapidissima	American shad
Alosa pseudoharengus	alewife
Brevoortia tyrannus	menhaden
Anchoa mitchilli	bay anchovy
Leiostomus xanthurus	spot
Menidia menidia	Atlantic silverside
Micropogon undulatus	Atlantic croaker
Morone saxatilis	striped bass
Morone americana	white perch
Perca flavescens	yellow perch

WILDLIFE (BIRDS)	
Anas platyrhynchos	mallard
Anas rubripes	black duck
Aythya valisineria	canvasback

The rationale for each of the weighting values follows.

- Sensitive to salinity. Since the major anticipacted effect of low flow conditions is an alteration of salinity regimes, this factor was weighted "4".

- Sensitive to circulation changes. Changes in circulation due to low-flow or altered salinity patterns can also be anticipated, and could affect distribution of some species. For this reason this factor was given a weight of "3".

- Sensitive to substrate. Substrate changes are not an anticipated major effect of low-flow, although the area of specified substrate within a certain salinity range will probably change. This factor was therefore weighted "2".

- Important to nutrient cycling. Although nutrient cycling is an important ecosystem function, the role many species play in it is not well-known. To reduce bias in favor of a few well-studied forms, this factor was only weighted "2".

- Affect water quality. A few species can cause deleterious changes in water quality (eg. algae blooms), and these might be enhanced by reduction in flushing rates due to flow flow. Since these effects will probably be local, this criterion was only weighted "1".

- Major biomass contributor. Biomass is not only a measure of a species importance or dominance in the ecosystem, a certain minimum level of abundance is necessary for a species to be useful as an indicator organism. Thus, this factor was weighted "3".

- Wide distribution in Bay. This actually means that a species with very restricted, localized distribution may not be a useful indicator. To minimize bias for very widespread eurytopic species, however, this criterion was only weighted "1".

- Rare and endangered species. Because of the restricted ranges and usually minor ecosystem impact of these species, this factor was rated "1". However, it was suggested that because of these organisms legal importance, the entire group should be handled as an entity in the assessment (see Chapter V, Section E).

- Trophic importance. Certain organisms are extremely important to the production and flow of energy through the estuarine ecosystem. Disruption of these species could have severe impact on other levels of the trophic web. For this reason, "Trophic Importance" was ranked "4".

- Specialized food requirements. Species with restricted food requirements at some point of their life cycle could be more severely affected by environmental perturbations than less specialized forms. Some species may themselves be eurytopic in regard to salinity, etc. but rely on a more stenotopic food species. This criterion was ranked "3" for the above reason.

- Major predator. Predation has been shown to be an important factor limiting distribution of many organisms. Change in distribution of a major predator might have significant effects on the Bay ecosystem, therefore this factor was ranked "3".

- Major competitor. Competition appears not to be as important in mediating organism distribution as predation, so this factor was ranked "1".

- Economic or social importance. Although these are the factors through which the public perceives the Bay's health, it was felt that the fact that an organism was economically important was not, *a priori*, a measure of that species' sensitivity to low flow. Many of these species do have life stages sensitive to salinity changes, or have predators or diseases which could be affected by low flow, but these species would receive high scores on those particular criteria. For these reasons, this factor was ranked as "1".

- Opportunistic colonizer. Species which are adapted to rapid colonization of disturbed habitats may respond quickly to habitat alterations due to low-flow. However, too high a ranking on this factor might bias the selection of species in favor of estuarine opportunitists, most of which are quite eurytopic. This factor received a "1" rating.

- Modifies habitat for other species. Species which provide habitat for other organisms (or conversely, which unfavorably alter habitat), can have significant ecological impact. This criterion was rated "2".

- Distribution data available. Pragmatically, it is necessary to have reasonably accurate and complete distribution information on a species to either map

it or to assess changes in distribution due to low flow. Thus this factor was heavily weighted as "4".

- Trophic data available. Complete and accurate information on a species' ecological importance is needed to assess what effects changes in its distribution might have on Bay's ecosystem. Thus, this factor was also heavily weighted, as "3".

- Sensitive life stages. Many species have a period in their life cycle which is potentially sensitive to environmental perturbation; this is typically a larval or juvenile stage. Although species which have such life stages will also score high on other factors (such as Sensitive to Salinity) it seemed better to also augment their score with an additional factor. This screening criterion was ranked "2".

This matrix-screening process produced a list of 57 study species. The list was distributed to the WESTECH review team, and presented at the March 20, 1980 conference for peer review. Input from the review process was used to generate the final list. In particular, the fish species were reevaluated in response to comments that life stages should each have been screened independently. Ranking each life stage separately changed the relative order to some of the candidate species, resulting in additions and deletions from the orginal list. One species which elicited wide-spread comment was the American shad, Alosa sapidissima. In light of its severely depressed populations, its suitability as a study species was questioned. However, the apparent current stresses on this fish are such that additional pressures due to low flow might prove critical, if such effects can be separated out and evaluated. Thus the species was retained as a study species.

Several benthic species were also reevaluated on the basis of comments, and additions and deletions were made. In particular, two species important in the oligohaline zone, the area where pronounced effects of low fresh water inflows are expected, were added, Gammarus daiberi and Cythaura polita. Corbicula manilensis was omitted due to its limited distribution, on the advice of reviewers.

The bald cypress (Taxodium distichum) was not retained as a study species due to its relatively restricted distribution. Stands of cypress which may be impacted by low flow will be evaluated on a site-by-site basis. Similarly, rare or endangered species, or others of special note, will be assessed on an individual basis.

The final study species list contains fifty-seven species and associations, including seven phytoplankton and three emergent vegetation associations, five submerged aquatic vegetation species, ten zooplankton, nineteen benthic invertebrates, ten fish, and three waterfowl. Each of these has been mapped, and their distribution in regard to salinity, season, substrate, etc. assessed. Predators (such as Beroe ovata) or diseases (MSX, "dermo") which are not themselves study species will be addressed in relation to the study species they impact.

Although fifty-seven species represent approximately 3 percent of the total Chesapeake Bay biota, these study species include many of the major organisms in the estuary. In addition, they are representatives of various salinity zones and estuarine habitats, and can serve as "models" for other species with similar requirements. Thus impact of low freshwater inflows can be assessed in a specific manner for the study species, and to a certain extent extropolated for the entire Chesapeake Bay ecosystem.

E. RARE, UNCOMMON OR THREATENED SPECIES

Selection of study species for the Biota Assessment has been carried out with consideration of eighteen factors which focus on importance of the organism to the Bay ecosystem (see Section V-D above). Due to the particular requirements of the Low Flow Project, the weighting criteria emphasized trophic and salinity categories and deemphasized such factors as economic importance

and rarity. Many of the economically important species were included in the final study species list because these species (mostly fish and shellfish) also rated high in other categories. Most of the Bay's rare or uncommon species, however, due to low scores in other categories, were not included as study species.

There are several rather clear reasons that uncommon species did not rate highly on a system geared toward salinity and trophic relationships:

- insufficient data (on distribution, feeding, salinity tolerance, etc.),
- not coupled tightly to estuarine system,
- minor quantitative importance in food web, at this time,
- Sensitive stages not well known.

Many rare or uncommon species are known only from a few sightings. Aside from organisms endemic to a certain portion of the estuary (i.e. bald cypress, Maryland darter), other organism distributions are known from a spotty, incomplete data base. Many are plants, birds or mammals which are often somewhat independent of the estuary and estuarine food webs. Plants such as bald cypress may be found both in estuarine waters and in non-estuarine freshwater swamplands in the Bay region. The southern bald eagle, while preferring estuarine habitat and food, does also feed on freshwater organisms or occasional terrestrial ones. Because of their rarity, these species cannot, by biomass alone, either predate or contribute in any major quantitative sense to the estuarine food web. The presense of bald eagles, for example, may be an important indicator of ecological health and productivity. However, these raptors cannot, due to their sparse populations, cause significant differences in the populations of fish or amphibians on which they prey. Additionally, because of their scarcity, and the justified reluctance of scientists to collect specimens of rare organisms, the life stages and physiological tolerance levels of many of these organisms have not been well studied.

Lists of rare or endangered plant species are published by the U.S. Fish and Wildlife Service. However, only vascular plants are considered. Maryland lists 9 and Virginia 43 (5 of which are overlapping) rare or endangered plants (Federal Register 40:127 pp27858, 27883-84). Of these, the majority are non-estuarine. A few such as alders (Alnus maritima), rushes (Juncus caesariensis), sedges (Carex biltmoreana, Carex chapmanii) and bulrush (Scirpus flaccidifolius) fall in the category of emergent aquatic vegetation; however, no submergent plants or non-vascular species have been enumerated. Submergent plants, while declining in many areas of the Bay, are not yet sufficiently scarce to be listed as endangered.

Another significant plant species, although not officially listed as threatened, is the bald cypress (Taxodium distichum). The northernmost outliers of this tree species occur in the southern swamps of Maryland and Virginia, including the Pocomoke in Maryland (Shea 1976) and the Chicahominy and other drainages in Virginia (Smithsonian Institution 1978). It is possible that low flow salinity changes may affect the distribution and success of the small outlier populations of this species in the Bay region.

Only a few animals are listed officially as rare or endangered by federal standards in Maryland or Virginia. Of these, the species associated with the estuarine ecosystems of the Chesapeake Bay include the Maryland darter (Etheostoma sellare) and the southern bald eagle (Haliaeetus leucocephalus leucocephalus). In addition, shortnosed and Atlantic sturgeon and Atlantic green, hawksbills, and ridley turtles have been historically important but recently reduced in the Bay. The other species are basically terrestrial in nature, although some (such as the Delmarva fox squirrel) occupy nearshore environments. In addition, species such as the osprey are present only in limited numbers or occupy goegraphical areas.

Many more species have been listed as rare or endangered by the states themselves. The Corps of Engineers, Chesapeake Bay Future Conditions report lists many of these species. Others

are contained in lists of endangered species published by the Maryland and Virginia Departments of Natural Resources. These lists expand the national lists through the addition of such species as shortnosed sturgeon, osprey, eastern brown pelican, Atlantic green and hawksbill turtles and many other aquatic species which may utilize Bay habitat.

Uncommon species, such as those listed above, were not included as study species for various combinations or reasons presented in this section. However, this in no way diminishes their importance or the vital ecological functions these organisms might perform if their numbers were to be increased. The Biota Assessment has used present conditions (1960's & 70's) as an environmental baseline; however, rare, uncommon or threatened species usually have both a genetic and ecological significance in their own right. While not discussed further here, these have been treated by others (see for example Clark 1977). Effects of low flow will be evaluated on a species by species basis.

F. DISCUSSION OF STUDY SPECIES

In order to more clearly explain the characteristics of each of the 57 study species, individual species discussions have been prepared. Due to their total length, these discussions cannot easily be included in the text. They have therefore been appended as Appendix A; however, the reader is cautioned that many of the textual discussionswhich follow may depend, to some extent, on knowledge of these species discussions. Below we present an outline of the main points included in the discussions of study species.

The study species discussions first define the most widely accepted common name(s) and identify the type of organisms (i.e. calanoid copepod, etc.). General range in the Bay and any seasonality of distribution or behavior are then discussed. Sensitivity to salinity or other potential effects of low flow

conditions form the focus of each species discussion.

For some species, relevant aspects of "potential habitat" are discussed. The purpose of this is to define habitat areas which may not have been completely documented on the literature, but which possess environmental conditions within which the species can survive. This is followed by a brief discussion of the species trophic importance. The discussion ends with a recapitulation of the particular selection factors which were of importance in the selection of the study species in question. See Appendix A for individual species discussion.

G. STUDY SPECIES DISTRIBUTION AND MAPPING

Mapping of study species was carried out on 1:250,000 scale, large-size (~33" x 54") base maps of the Chesapeake Bay. These maps are in the Map Atlas which is on-file with the Baltimore Corps of Engineers. The purpose of this mapping was to provide an atlas of species distribution under base year (1960 - 1961; see Chapter IV) salinity conditions. The upstream limit of all mapping was defined to be the head-of-tide in each tributary (see Figure IV-2) and the downstream limit was the Bay mouth. Within this area, basemaps were prepared, using differing density shading films to indicate distribution of species and/or populations (depending on organism type). In many cases, the data permitted the elucidation of seasonal shifts in distribution or abundance, migration and other pertinent factors. Figures V- 1 - V- 2 are reduced-scale examples of some of the map characteristics. Mapping technology and techniques were to a considerable extent patterned after Lippson (1973).

In some cases, it was possible to differentiate "known" versus "potential" habitat (see section II-E). Sparcity of detailed field data precluded doing this with more species. Fish, for

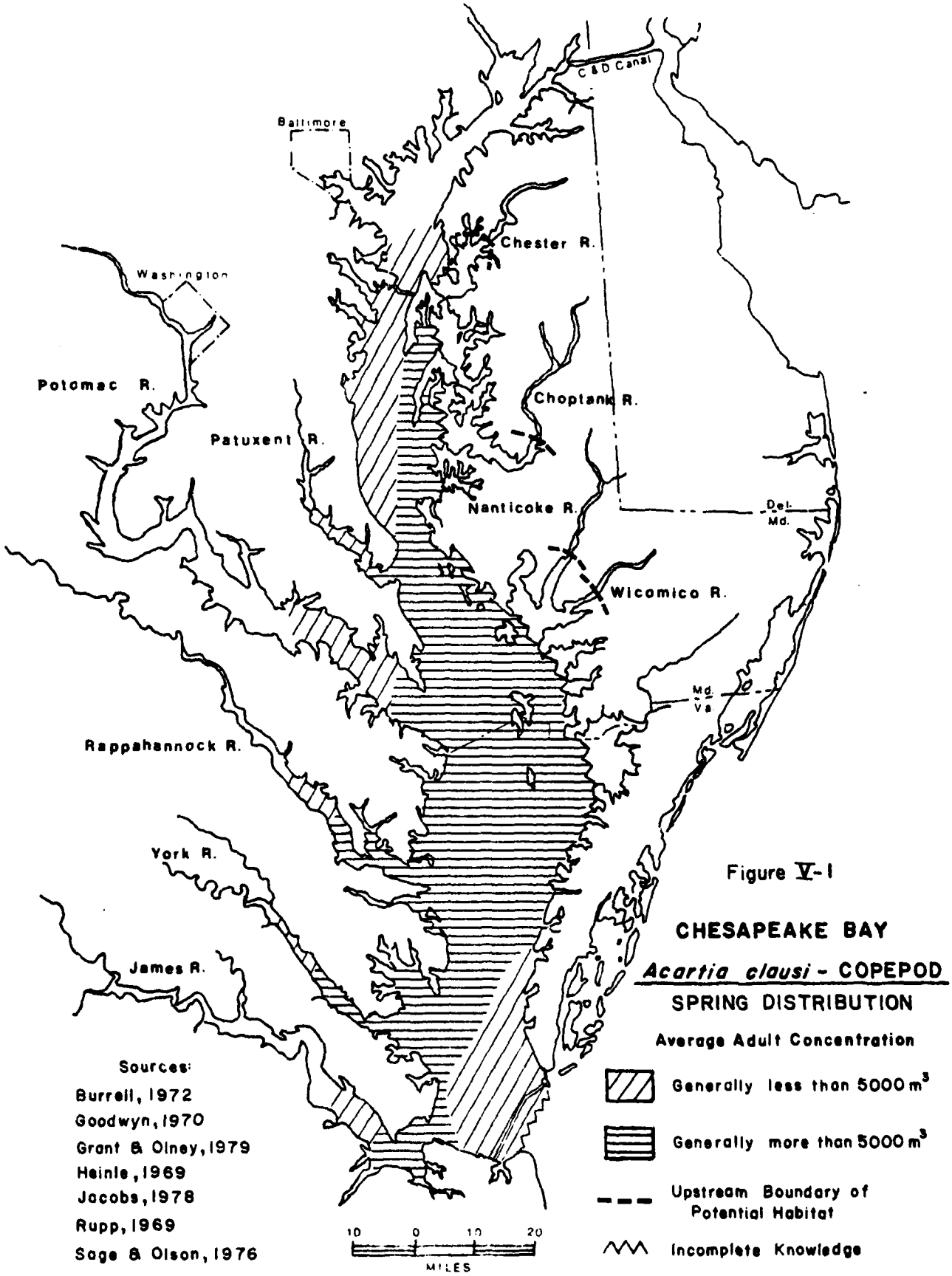

Figure V-1

CHESAPEAKE BAY

***Acartia clausi* - COPEPOD**

SPRING DISTRIBUTION

Average Adult Concentration

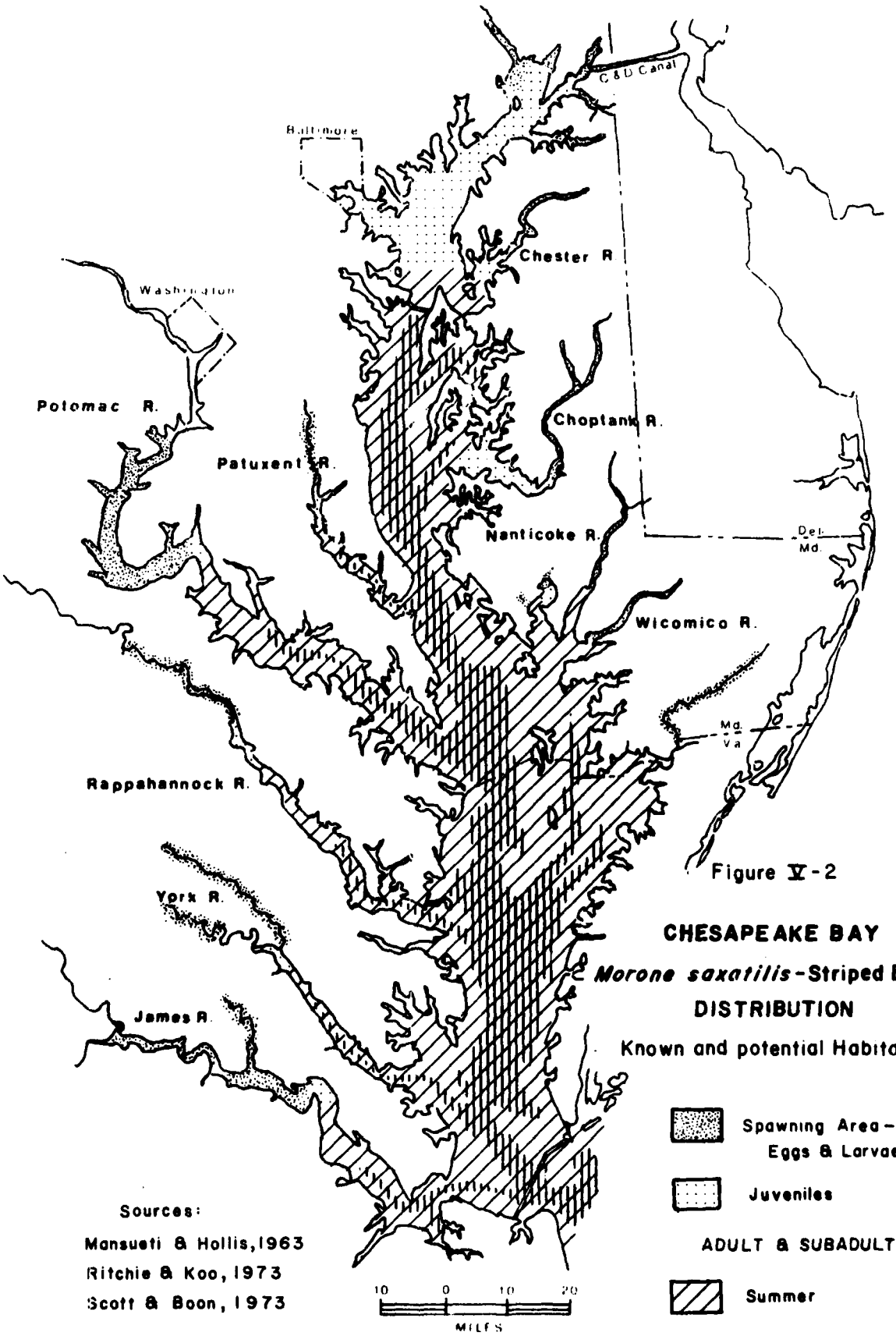

Figure V-2

CHESAPEAKE BAY

***Morone saxatilis*-Striped Bass**

DISTRIBUTION

Known and potential Habitat

example, have seldom been sampled on a large-scale geographic basis with consistant methodologies. In many cases, extensions of information on known behavior, location and salinity tolerance were made into areas in which no data exists. This is particularly true for most of the eastern shore tributaries, which have been studied very little in comparison with western shore rivers.

The mapping process consisted of several steps. Species distribution was first determined from existing field studies, aerial surveys, map surveys, and other literature or information bases. Points or areas where organisms were present or absent were recorded precisely on base maps and color-keyed to the source study. In most cases compilation of the Baywide map for each study species was the result of the juxtaposition of many studies, each on an individual tributary or Bay segment. Then, since each individual study typically came from differing years or time periods, it was sometime necessary to adjust the upstream or downstream limits of species distribution to the "base year", predicated on field data on organisms salinity tolerances. The mapped locations and abundances thus represent a best judgment base-year distribution. Since there is no one year in which all species have sampled, this was found to be necessary standardization procedure.

The salinity information which formed the basis for this standardization was plotted on full sized basemaps in the form of lines of equal salinity values (isohaline) derived from the Chesapeake Bay Institute slack-water runs up the Bay main-stem as reported in the Chesapeake Bay Salinity Atlas (Stroup and Lynn 1963). Tributary salinity values were obtained from state or federal data bases, from biological studies, or interpolated or extrapolated from known values. Where fish or benthic surveys also reported salinities and station location, these salinities were plotted and used in defining isohalines. Very limited salinity information exists on eastern shore rivers during the base year (1961). For this reason, it has sometimes been necessary to substitute data from other years.

Wherever organism distribution is mapped from non-base year data, this has been noted on that species map.

Depth, substrate and presence of other organisms has also been used to define species distributions. Species have been classified into known suitability for certain mappable substrates (sand, muddy sand, etc.) and for certain depth categories (0 -3, 3 - 6, 6+ meters). Other species are known to coexist with such organisms as particular groupings of submerged aquatic veteta-tion. Base-maps for these parameters have been used to define or adjust potential habitat wherever applicable.

All mapping of salinity (as well as depth and substrate to some extent) represents a "snapshot" taken of a continuous process. The isohalines shift with the state of the tide, seasonally, and from year to year. The maps show species boundaries along base-year isohalines (Venice boundaries) in order to provide means of quantifying the distribution of study species. It should be understood that during other seasons or years organisms may be found outside of the mapped boundaries, while still occupying the potential habitat indicated by these base-year maps. The maps should be read as if the organisms had been synoptically sampled at high-slack water during a particular season of 1960 and 1961 (Water Year 1960).

Most of the groups mapped were found to have certain character-istics peculiar to the organism group or the ways in which it has been historically sampled. Planktonic organisms are often mapped as associations since distribution patterns of many of the species making up these groups are little known. Since these organisms are predominantly affected by water character-istics, seasonal maps were prepared in all applicable instances. Substrate, depth and other organisms were not usually important factors for determining plankton distribution.

For benthic organisms in particular, substrate, depth , salin-

ity and other organisms are often all important factors in determining distribution. Prior history of a site or area can also be relevant. It should be remembered, for example, that the base-year period preceded the effects of Tropical Storm Agnes, and contemporary benthic distributions may be displaced downstream from mapped distributions. In other cases, benthic surveys are even farther out-of-date. The Maryland oyster grounds survey was last completed during 1909 - 1913, and significant changes have occurred in the location and extent of oyster bars since that time. Virginia has completed an updated and much more accurate resurvey (Haven et al. 1977, 1979, 1980) and Maryland is attempting to resurvey at the present time.

Submergent and emergent aquatic plants have both had large-scale surveys completed in recent years. A Baywide survey of submerged aquatic vegetation, using aerial photography (remote sensing) has been recently completed. These data serve as the basis for SAV mapping. Each of the bay states surveyed wetlands in the 1960's and early 1970's. Wetland inventories required two years (Maryland) to nearly a decade (Virginia) to complete. Emergent vegetation was mapped from these county by county wetland surveys.

Nekton (mainly fish) were mapped by sequential aggregation of studies. Maps were prepared of estuarine segments where studies have been conducted. Sampling stations were plotted and coded by presence or absence of the species, as well as abundance categories where data were available. When density or abundance information was collected, the sampling points were color coded into density ranges. The sectional maps were then pieced together to make a rough-copy basemap. The rough basemap of known distributions was next examined with respect to Venice boundaries, depth, substrate type, etc., which delineate potential habitat and necessary minor adjustments made. The final maps were then created from the rough basemaps.

Aerial surveys by state management agencies (Maryland Wildlife Administration and Virginia Fish and Game Commission) were used to define waterfowl distribution. Data from 3 to 5 year averages were obtained wherever possible, since waterfowl data showed wide fluctuations from year to year. Birds were counted by census tracts set up by the agencies. These tract counts were reaggregated into Bay modeling segments and mapped by density of birds per 100 square kilometers.

In Phase II, the Map Atlas will be supplemented through maps of organisms distributions based on average inflow (modal hydrograph) and drought scenario salinity data from Corps of Engineers hydraulic model. The species selection and mapping described in this chapter will not only provide a data base in its own right, but will also provide a reference point for assessing the relationship of hydraulic model data with actual historical base-year distributions.

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VI. THE CHESAPEAKE BAY ECOSYSTEM MODEL

This chapter describes the third major conceptual component of methodology developed during Phase I, that of ecological modeling. Such modeling can, in theory, range from the setting of a conceptual framework, to the creation of a complex dynamic mathematical computer model, as the data permit. The extent to which these approaches are appropriate depend on the availability and accuracy of data on ecosystem interactions. However, some form of modeling, be it comceptual or mathematical, is necessary to order, group and understand the numerous complex interactions which comprise an estuarine system as large and diverse as Chesapeake Bay. For this reason, concurrent with habitat classification, definition of salinity tolerances and other methodological tasks (see Chapters IV and V), WESTECH developed first a conceptual framework (model) of the Chesapeake Bay ecological system focusing on trophic relationships. From this conceptual basis, drawing extensively on the scientific Bay literature, a mathematical simulation model of the Bay was developed.

A. INTRODUCTION

One of the objectives of the Chesapeake Bay Low Flow Study is to quantify, to the extent possible, differences in the productivity and functioning of biological systems due to changes in salinity, due to decreased freshwater inflow. To this end, WESTECH has developed impact evaluation strategies based on potential habitat differences and conceptual modeling and ecosystem simulation. In this chapter, the development and structure of the conceptual and mathematical model are discussed. The structure and capabilities of the computerized math model are also discussed, as are the limitations of ecosystem simulation. Several one-year simulations of the Patuxent estuary using the Chesapeake Bay Ecosystem Model (CBEM) are also included in this chapter. Finally, several simulations of alternative salinity scenarios in the Patuxent estuary are included to demonstrate the utility of the CBEM as a tool in understanding salinity-based ecosystem modifications.

A computer simulation of an ecosystem attempts to reproduce some function of that system, while at the same time basing the simulation on a simplification of the ecosystem structure (Hall and Day 1977). Structure includes the biotic as well as the abiotic components, which in real ecosystems become so numerous and the relationships so complex that simplification is essential. Indeed, it is doubtful whether all the species in any natural ecosystem have been identified and counted; certainly all the relationships between components are not known for any ecosystem. However, it is doubtful that such complete detail of information is necessary for computer simulation to be a useful tool (Patten 1971). There are many species in biological systems whose abundance is such that they seem to contribute little to the trophic schemes usually used in modeling, although some of those species will be important in regulating ecosystem processes (Kuenzler 1961, Connell 1961). This is not meant to minimize the importance of such species in long-term ecosystem development (Darwin 1859) but to point out that daily and seasonal processes are often dominated by a few abundant species. In any event, computer simulation, as well as much ecological research, involves aggregating species into trophic assemblages where more or less general storage and transfer rates are used to describe the assemblages and their inter-relationships. This trophic-dynamic view of ecology (Lindeman 1942) can support considerable theoretical analysis (Ulanowicz and Kemp 1979).

A computer simulation of an ecosystem is a tool. Reproducing ecosystem function while being able to manipulate the components can provide insight in several directions. Ecological theory can be explored with general simulation models (Kemp and Mitsch 1979, Geritsen and Strickler 1977) while simulation of a specific ecosystem aids in understanding processes in that system as well as yielding insights into the more general aspects of ecosystem function (Kremer 1978, Anderson and Ursin 1977). Finally, computer simulation can be used to predict changes in the structural or functional aspects of an ecosystem based on the manipulation of important parameters. This is probably the most difficult use of computer simulations since such a model should be run using independent data that was not used to initialize the model (Ulanowicz et al. 1978).

A number of simulation models directed toward biological objectives have been or are being developed for the Chesapeake Bay. Simulation models are being developed to investigate various aspects of submerged aquatic vegetation in the Maryland Bay (Stevenson et al. 1979) and in the Virginia section (Wetzel et al. 1979) as a part of the U.S. Environmental Protection Agency's Chesapeake Bay Program. Other EPA related model development in the Chesapeake Bay includes the modeling of Bay circulation (Shubinski 1979) and the development of models to identify factors affecting eutrophication in the Bay (Ambrose 1979). Ulanowicz (1976) has reviewed much of the hydrologic modeling literature important to the Chesapeake Bay. O'Connor et al. (1975) applied a model of phytoplankton dynamics to the Potomac estuary. Their model placed much emphasis on problems of eutrophication in the Potomac. Numerous biological models have been developed for other aquatic ecosystems, such as Narragansett Bay (Kremer and Nixon 1978), the North Sea (Anderson and Ursin 1977), the Scramento-San Joaquin Delta (Di Tora et al. 1971) and others.

The Chesapeake Bay Ecosystem Model, in conjunction with mapped distributions and abundance information, is being used in the Biota Assessment to help understand the patterns and interrelationships of species under modified salinity regimes. CBEM is not meant to automatically predict the changes that occur when salinity regimes are modified. Rather it is used heuristically in that a number of expected, specific changes, such as respiration or predation rates, can be programmed and CBEM will integrate them into the system. The resulting patterns are then analyzed and interpreted in the light of the information known about the real Chesapeake Bay.

To properly integrate this information, CBEM must simulate a number of locations throughout the Bay where initial physical and biological conditions differ substantially. A primary objective, however, is to keep the number of necessary segments to the minimum required to estimate the effects of salinity changes (Ulanowicz and Neilson 1974). Toward this end, the Bay has been divided into thirteen segments (Figure VI-1).

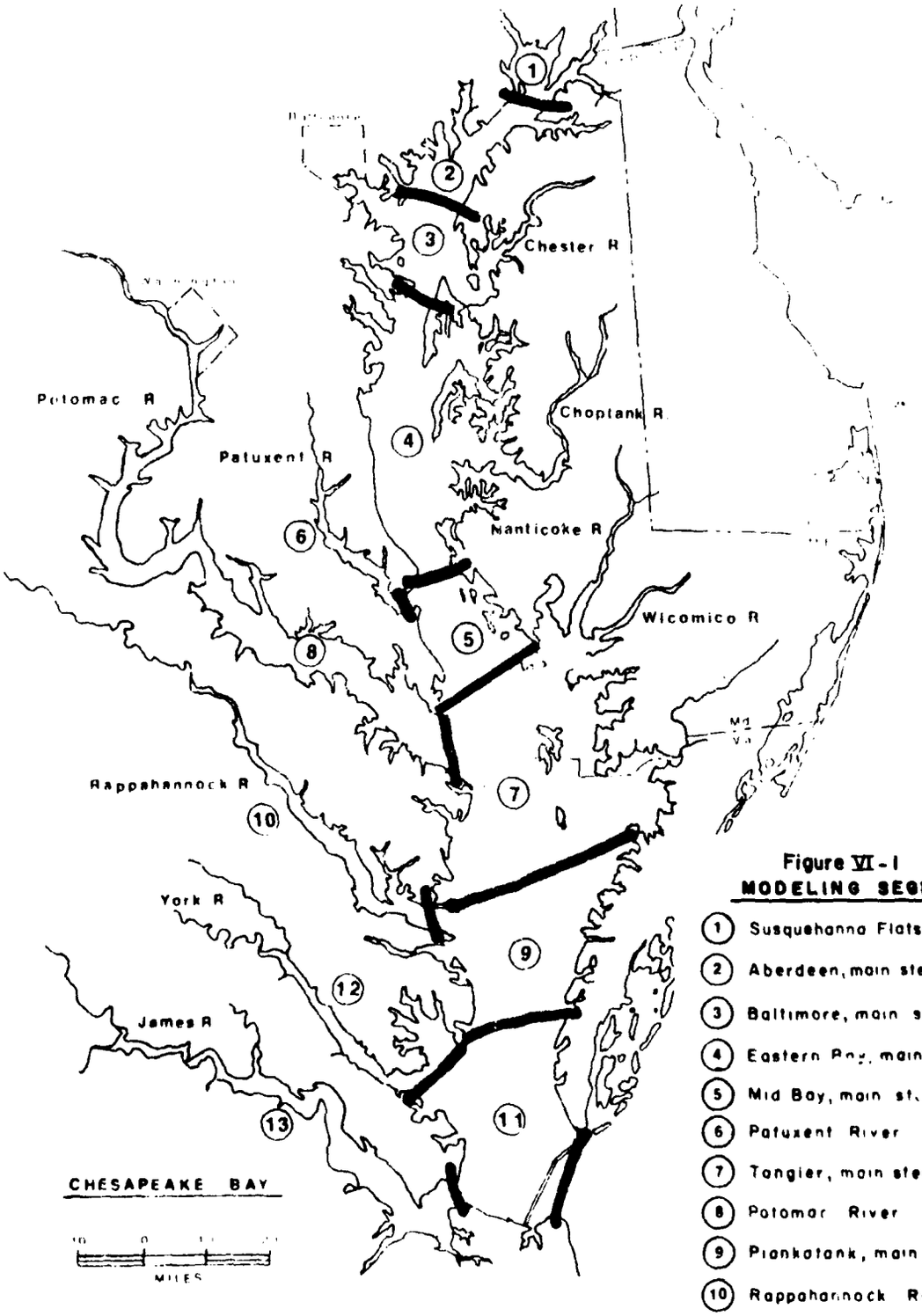


Figure VI-1
MODELING SEGMENTS

1. Susquehanna Flats, main stem
2. Aberdeen, main stem
3. Baltimore, main stem
4. Eastern Bay, main stem
5. Mid Bay, main stem
6. Patuxent River
7. Tangier, main stem
8. Potomac River
9. Pianketank, main stem
10. Rappahannock River
11. Bay Mouth, main stem
12. York River
13. James River

Except for the Susquehanna River segment (#1), which includes the flats, each of the major western shore rivers comprise a segment. The remaining segments are comprised of the mainstem of the Bay, including the eastern shore rivers. Each mainstem segment has only one western shore tributary feeding into it. Locations of pertinent salinity changes within these segments will be selected for simulation in Phase II of the Biota Assessment. In the sections below we summarize the development of CBEM, beginning with conceptual bay models.

B. CONCEPTUAL MODELS

Intensive compartment models of the Chesapeake Bay were formulated through a process of studying one trophic aggregation or compartment at a time (i.e. net-phytoplankton, macrozooplankton, demersal fish, etc.). This process began by defining sources of food and energy, predators, life stages, seasonal migratory behavior, requirements for nutrients and other interactions for each compartment. From these very detailed compartment models (not shown) a simplified conceptual model of the Chesapeake Bay was constructed (Figure VI-2). The symbols used in the conceptual model are defined in Figure VI-3.

The conceptual model shown illustrates the flow of energy from the sun through the plants and animals of the ecosystem. Also shown is the movement of nutrients and non-living particulate matter through the ecosystem. In the model, radiant energy is used by four primary producers compartments (net phytoplankton, nannoplankton, submerged aquatic vegetation, and emergent aquatic vegetation) to produce plant tissue. Two of these plant compartments, net phytoplankton and nannoplankton, produce material which primarily enters a grazing food web. Zooplankton, both macro- and micro- (copepods, rotifers), feed on these plants, as do icthyoplankton, invertebrate meroplankton (oyster, barnacle larvae, etc.), forage fish and menhaden. Benthic suspension feeders also graze the phytoplankton.

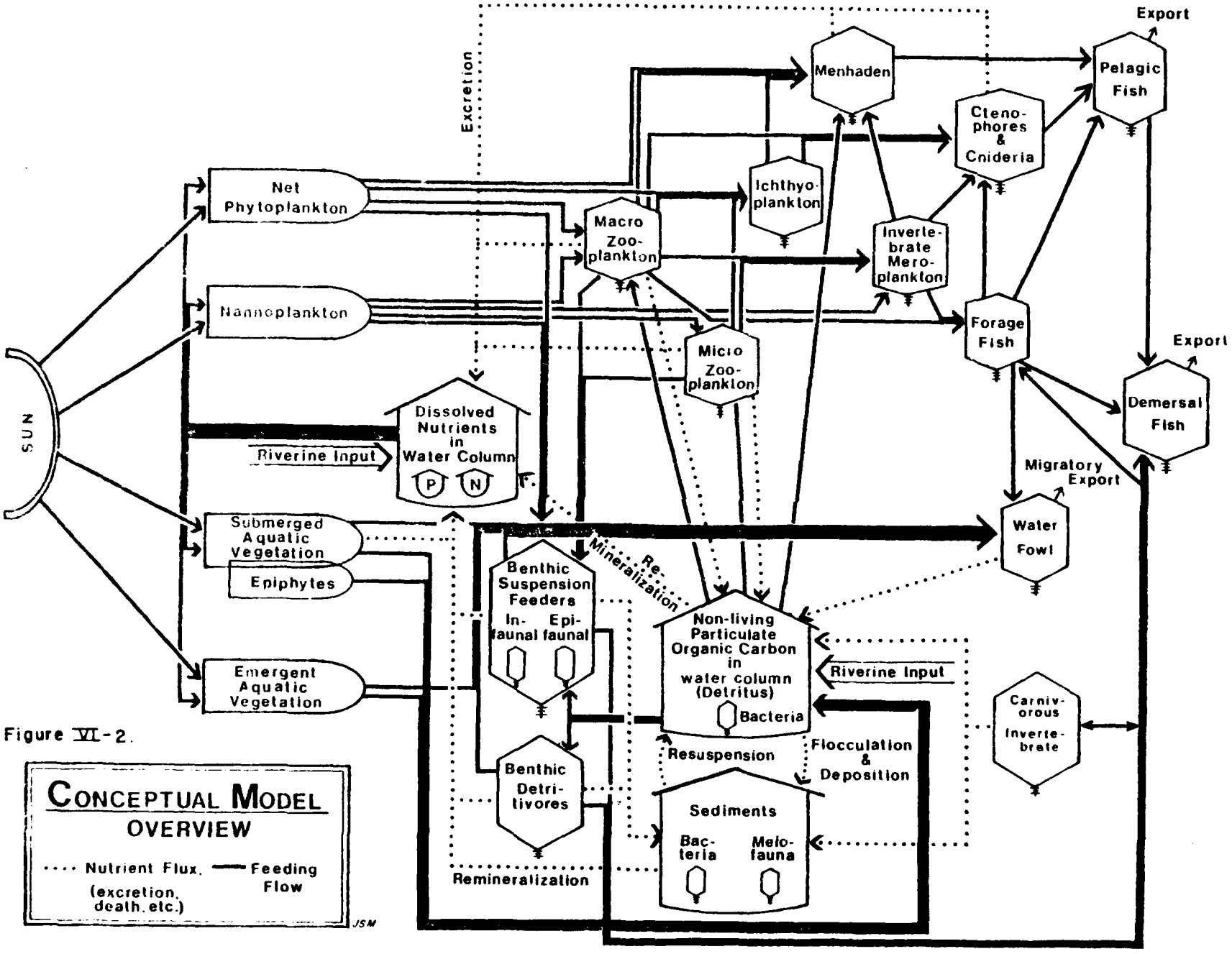

Export
Excretion
Menhaden
Pelagic Fish
Ctenophores & Cnideria
Ichthyoplankton
Net Phytoplankton
Macro Zooplankton
Invertebrate Meroplankton
Nannoplankton
Forage Fish
Micro Zooplankton
Export
SUN
Dissolved Nutrients in Water Column
P
N
Riverine Input
Demersal Fish
Migratory Export
Water Fowl
Submerged Aquatic Vegetation
Epiphytes
Re-Mineralization
Benthic Suspension Feeders
In-faunal
Epi-faunal
Non-living Particulate Organic Carbon in water column (Detritus)
Bacteria
Riverine Input
Emergent Aquatic Vegetation
Carnivorous Invertebrate
Resuspension
Flocculation & Deposition
Benthic Detritivores
Sediments
Bacteria
Meiofauna
Remineralization
CONCEPTUAL MODEL
OVERVIEW
Nutrient Flux. (excretion, death, etc.)
Feeding Flow
JSM

Figure VI-2.

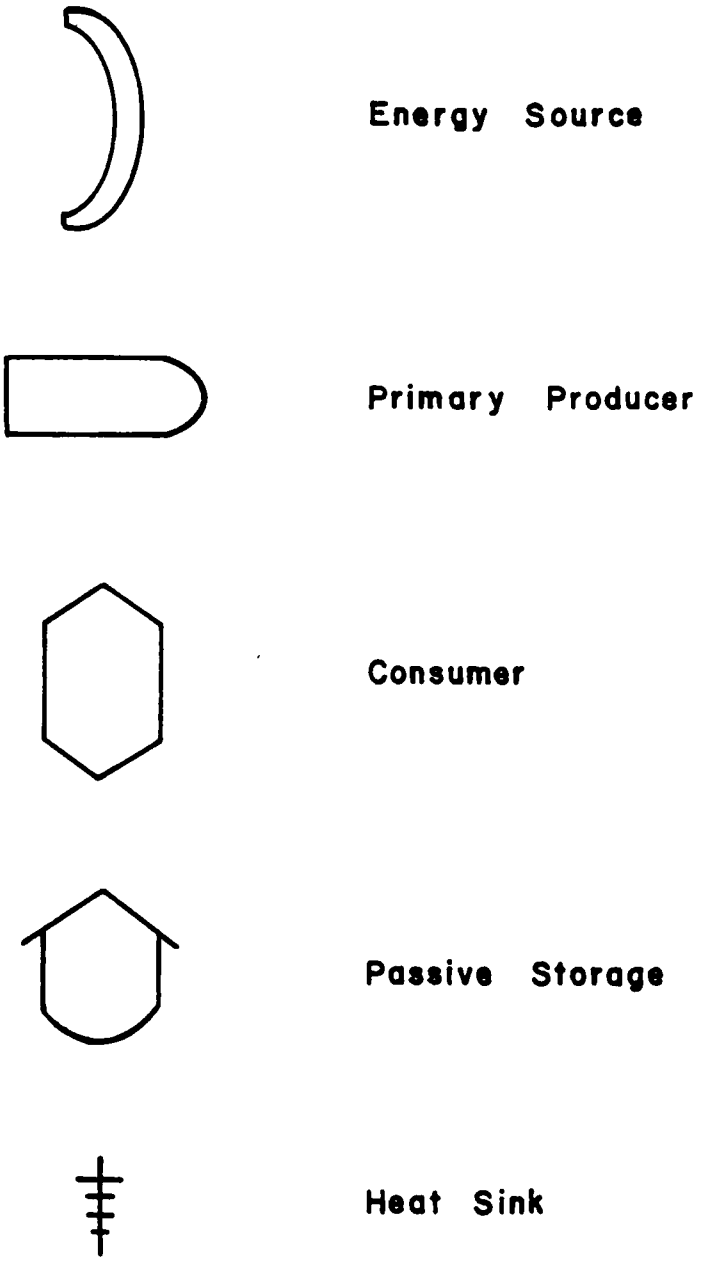


Figure VI-3

KEY TO SYMBOLS USED IN THE CONCEPTUAL MODELS

Source: Odum, 1972

The other two primary producer compartments, emergent aquatic vegetation and submerged aquatic vegetation (which includes a smaller epiphytic community) contribute the major portion of their production to the detrital food chain (although a substantial amount is eaten by waterfowl). The detritus produced is utilized by benthic detritivores (crabs, etc.) and benthic suspension feeders (oysters, clams, etc.). Macrozooplankters, forage fish, and menhaden also utilize detritus to a certain extent.

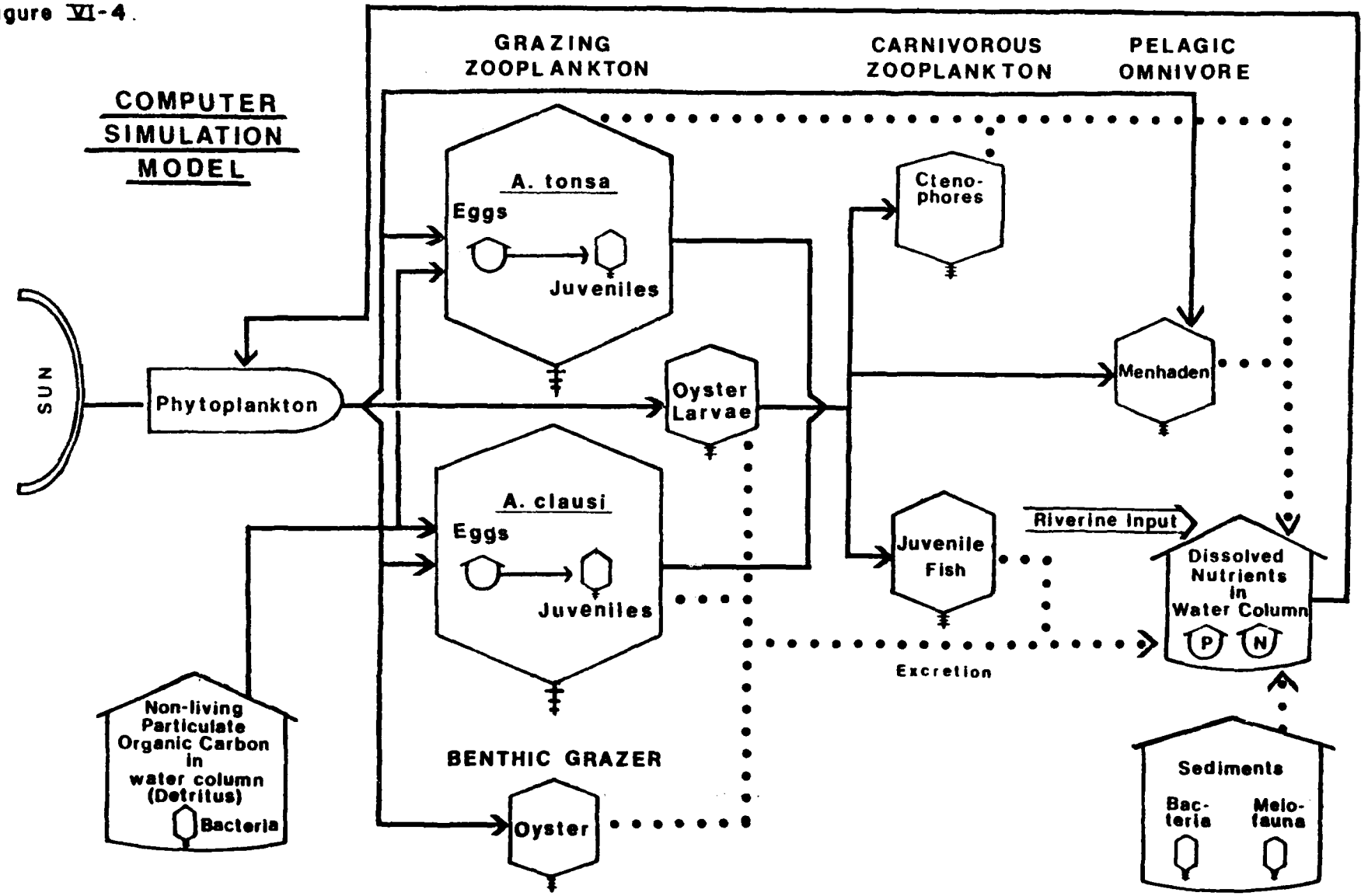
The plankton species mentioned above (macro- and micro-zooplankton, icthyoplnakton, and invertebrate meroplankton) are fed upon by ctenophores and cniderians (comb-jellies and sea-nettles), fish such as menhaden and forage fish (silversides, etc.), and benthic suspension feeders (such as barnacles). At this point in the conceptual model energy flows to the predator layers of the system. Pelagic fish (bluefish, etc.), demersal fish (flounder, etc.), and waterfowl (canvasbacks) are top predators, and the energy equivalent of the food they eat is exported from the system or expended in feedback controls in the system.

The original intent of the mathematical model development was to simulate the interactions shown in the entire conceptual model through the use of "key" species and interactions. As refinement of the conceptual model progressed, two factors emerged to modify this approach. First, it became clear that the number of necessary key species throughout the Bay would be too large (on the order of 50 species or more) to carry out economical computer simulations. Secondly, community variation in different geographic regions of the Bay made selection of Baywide key species difficult. To solve these two problems and based on suggestions by anchor team members, we elected to focus on specific areas of the Bay, modeling mathematically key communities which are subcomponents of the overall conceptual model. One such area was selected for development and calibration of the mathematical model. As previously stated, the mathematical computer model designed by WESTECH was developed to help predict the responses of an ecosystem to salinity changes.

The Patuxent River has been found to have one of the most complete and consistant biological data bases in the Chesapeake Bay (Mihursky and Boynton 1978). Hence, this area provides a data source with which to calibrate and verify the model with accurate historical data for a number of species and compartments. Therefore, the model was developed based on selected organisms known to inhabit the lower (mesohaline) reach (see Figure IV-16) of the Patuxent estuary. During Phase II of the Study, the model is expected to be applied to other zones and other key geographical areas of the Chesapeake Bay.

The final conceptual model used as a basis for the mathematical model is shown in Figure VI-4. Considerable simplification has occurred in this model as compared to the conceptual model in Figure IV-2, but the biological components most critical in estuarine analysis have been included. The phytoplankton, zooplankton (represented by Acartia tonsa and A. clausi) and the ctenophores (represented by Mnemiopsis leidyi) are fully interactive components of the model. The remaining compartments are present as forced drains, although when feedback from the interactive components to a forced compartment is considered critical it will be made interactive. In effect, the forced compartments represent a built in flexibility of the CBEM, since simulations of varied Bay segments can be accomplished relatively rapidly by modifying the forced compartment and the relevant abiotic drivers (discussed below).

Figure VI-4.


COMPUTER SIMULATION MODEL
GRAZING ZOOPLANKTON
CARNIVOROUS ZOOPLANKTON
PELAGIC OMNIVORE
A. tonsa
Eggs
Juveniles
Ctenophores
SUN
Phytoplankton
Oyster Larvae
Menhaden
A. clausi
Eggs
Juveniles
Juvenile Fish
Riverine Input
Dissolved Nutrients in Water Column
P
N
Excretion
Non-living Particulate Organic Carbon in water column (Detritus)
Bacteria
BENTHIC GRAZER
Oyster
Sediments
Bac-teria
Melo-fauna

C. MATHEMATICAL AND COMPUTER MODELS

1. The Mathematical Representation for the CBEM

CBEM has been programmed in Fortran V for use on the UNIVAC 1108 system. All model runs have been conducted using the University of Maryland 1108 Reentrant Algorithmic Processor (designed RALPH) compiler system. Some subroutines are programmed in Univac Assembler coding. Standard Univac graphical packages are coupled to CBEM for display of data.

The theoretical basis for CBEM assumes that the main aspects of the instantaneous state of the ecosystem are represented by a vector X containing components x_1, x_2, x_3, ... x_n, each of which represents the energy or biomass of a species at one instant of time (Patten 1971). Changes in the biomass of each species (growth or decline) are governed by factors of food (or energy) availability, excretion and death under the environmental conditions present. In a mathematical model, changes in a species x are represented by the symbol x_1, which generally depends on the species itself (X_1), other species (x_2, x_3, etc.) and in some cases physical driving factors directly (i.e. sunlight, nutrients). These relationships can be summarized in a differential equation of the form:

$$\dot{x} = \quad f_{o1} + ax_1 + bx_2 + ... nx_n$$

where the coefficients a, b, etc. are each made up of rate relationships for assim lation, respiration and other factors. In this context, the state of the entire system becomes a <u>set</u> of coupled differential equations which represent the changes over time of x_1, x_2 . . . . x_n. In many cases, the terms in these equations are found to depend on more than one organism (i.e. terms of the form $ax_1\ x_3$etc.). This effect makes the differential equations non-linear and hence somewhat difficult to deal with computationally.

In CBEM, we use a system of coupled quasi-linear differential equations of the form:

$$\dot{x}_1 = f_{01} + a_{11} x_1 + a_{12} x_2 + a_{13} x_3 + \ldots a_{1n} x_n$$
$$\dot{x}_2 = a_{21} x_1 + a_{22} x_2 + \ldots a_{2n} x_n$$
$$\dot{x}_3 = a_{n1} x_1 + a_{n2} x_2 + \ldots a_{nn} x_n$$

where each coefficient "a" is determined by combining rates of assimilation, respiration, excretion, death and other factors (import, export, etc.) derivable from the literature. In cases where there is dependence on more than one species per term (non-linearity), a quasi-linear approach to the numerical integration has been used. The non-linear term is "disguised" as a constant within the system of linear differential equiations but is periodically recomputed outside of the equation set. Hence these disguised constants are reset periodically but do not introduce direct nonlinearity into the equations. The constants are manipulated to form part of the a_{ij} or part of the driving functions f_{ij}.

The differential equation set is solved by numerical integration techniques using a canned Runge-Kutta numerical integration package. The advantages offered by this particular method include use of a variable time step and a flexibility in calculating the future condition of the system independent of its past evolution. This permits rapid solution of the equations even during periods of rapid growth or reduction of certain species.

2. The Model Drivers (Light, heat and nutrients)

Light, heat and nutrients are the basic abiotic parameters in any ecosystem. Light is used by photosynthetic organisms to fix carbon into organic molecules. The plant material produced is the basis for the entire trophic structure of the ecosystem. Plant material is eaten and the energy released is used to build animal tissue in both grazers and carnivores. Fecal material and dead animal and plant cells supply energy to decomposers.

The ambient temperature of the environment directly or indirectly controls the rates of biological (and non-biological) reactions. Photosynthesis, respiration, and ingestion can be controlled by temperature, as can various reproductive processes. Adaptations to long-term (seasonal), predictable changes in temperature by the biota contribute to large scale patterns in ecosystems (Slobodkin and Sanders 1969).

Nutrients are components of a great many molecules critical to the physiology of living organisms. Nitrogen, found in proteins, lipids, nucleic acids, chlorophyll and other molecules; and and phosporus, a component of proteins, lipids, nucleic acids and high energy molecules such as ATP, are often limiting to the organisms in an ecosystem.

In CBEM, nutrient values are input for the particular river basin from data either as initial values which are then acted upon by the biota, or as periodically corrected values based on seasonal nutrient values. Nutrients are presently represented as total nitrogen and phosphorus or as the limiting nutrient although it is possible to use subcategories (i.e. ammonia nitrogen) where data exist. Nutrient values change through time due to seasonal changes in input or through interactions with other biotic or abiotic compartments in CBEM.

Light: For the Patuxent River simulation, long-term incident solar radiation data taken at the Patuxent Naval Air Station was used (Cinquemani et al. 1978). A smooth curve was generated from this data to provide daily radiation inputs into the phytoplankton compartment. With such a smooth average curve, daily fluctuations in incident radiation due to cloud cover are, of course, lost. These fluctuations appear to be most important when phytoplankton light acclimation is considered (Kremer and Nixon 1978).

The effects of variable light intensity on phytoplankton populations in the field is unclear however (Steel 1974), and not all apparent light acclimation is due to changes in the photosynthetic response to changed light intensities (Yentsch and Lee 1966). Because light acclimation by phytoplankton is not a part of the CBEM, no daily variability has been provided in the sunlight input.

The rate at which light is attenuated as it moves through the water column is affected both by living and non-living material. The living component is assumed to be chlorophyll and chlorophyll-related substances, while the non-living component includes both the water and substances in it (Riley 1975). Riley's (1956) equation relates phytoplankton chlorophyll to the total extinction coefficient of water:

$$k = k_w + 0.054C^{.667} + 0.0088C$$

where k = total extinction coefficient of water (m^{-1})

k_w = extinction coefficient of water with no chlorophyll (m^{-1})

C = chlorophyll *a* concentration (mgm^{-3})

k_w values are important in the model when calculating the total extinction coefficients (k) produced as a result of increases in the phytoplankton compartment (this self-shading factor is discussed below). To determine k_w values back-calculations were done using the above equation and published values for chlorophyll *a* and extinction coefficients (Flemer and Olmon 1971, Whaley *et al.* 1966).

Nutrients: Nutrient levels in the sub-estuary depend upon loading rates from run-off, inputs from the sediments, and uptake and excretion by the organisms present. Nutrient loadings of

nitrogren and phosphorus are comprised of point and non-point sources (Correll 1976). Point source loadings remain relatively constant over time while non-point source loadings may be closely tied to run-off (Clark et al. 1973).

Dilution and freshwater run-off effects on nutrients provide a means of manipulating the nutrient input to the phytoplankton compartment during base year flow and low flow simulations. However, published nutrient budget data for the Chesapeake Bay and individual sub-estuaries are not yet adequate to accomplish this in a satisfactory way (Heinle et al. in press, Mihursky and Boynton 1978); however, best possible estimates will be used. Since the lower Patuxent and other Bay sites are two-layered systems during part of the year, we plan to modify a flusing equation based on salinities (Kremer and Nixon 1978) to develop the capability to simulate nitrogen and phosphorus mixing in and between the model segments.

Nitrogen and phosphorus regeneration from the sediment can also significantly affect the overlying water, especially in shallow estuarine systems (Pomeroy 1975). Regeneration is correlated with temperature, and variations in nutrient output between disparate community types may be minimal (Hale 1975). Sediments may supply approximately 30% of water column nitrogen demand (Boynton et al. 1977). Benthic nitrogen regeneration in the CBEM is based on temperature:

$$N = N_o + 116.5\ (8.66T - 34.9)$$

although other facets of the nitrogen budget, such as nitrogen fixation and denitrification, are still being examined.

Temperature: Temperature is important in the CBEM, acting as an external interactive variable in almost all compartments. Temperature acts as a switch for a number of organismic processes, including the onset of feeding and reproduction,and the development time of eggs and larvae (see below). The temperature inputs to the model are from long-term data taken in the Patuxent estuary (Ritchie and Genys 1975).

3. The Model Compartments

Phytoplankton: The phytoplankton compartment is driven by temperature to reproduce at a maximum rate. This maximum reproductive rate is then decreased by light and nutrient limitations (Kremer and Nixon 1978, DeToro et al. 1971). Eppley's (1972) growth equation:

$$\log_{10} u = 0.0275 \text{ Temperature} - 0.070$$

where u = divisions per day (maximum) at the specified temperature, is converted to the base of natural logarithms in order to get an instantaneous growth coefficient (Kremer and Nixon 1978):

$$r_{max} = 0.59e^{0.0633T}$$

where r_{max} = the maximum instantaneous growth rate, at the specified temperature.

In the CBEM the equation has been changed somewhat to decrease the growth rate below 5°C in order to account for the warmer water species present in the Chesapeake Bay (Patten et al. 1963).

The maximum growth rate (r_{max}) occurs when there are no other factors limiting the population. Realized growth rate occurs when there are other environmental factors acting upon the population (Krebs 1972, Odum 1971). The two most important factors (besides grazing) are light and nutrients.

The maximum growth rate (r_{max}) is reduced by the following equation to account for the effects of variable light intensity:

$$\frac{r}{r_{max}} = \frac{eF}{KZ}\left[e^{-\frac{I}{I_{opt}}e^{-KZ}} - e^{-\frac{I}{I_{opt}}}\right]$$

where r = realized growth rate
K = extinction coefficient
Z = depth
F = photoperiod as a fraction of the 24-hour day
I = incident radiation
I_{opt} = optimal light intensity

This equation integrates the effect of non-optimum light conditions both with depth and with the time of day. In a column of water there will be a point where the amount of light reaching the phytoplankton is optimum; however, above or below this point photosynthesis will decrease due to inhibition by too much light or decrease due to insufficient light. This depth of optimum light will change as the day progresses. I_{opt}, the light intensity at which the photosynthetic rate is maximum, ranges from 0.1 to 0.2 calories/cm^2 per minute from spring to late summer in the model, to account for the increasing dominance of dinoflagellates over diatoms at this time (Lehman et al. 1975, Eppley and Strickland 1968).

The increased light attenuation in the water column due to phytoplankton growth provides immediate self-regulating feedback to the phytoplankton compartment (Kiefer and Austin 1974). In the model, the equation of Riley (1956) previously discussed in relation to calculating k_w (the extinction coefficient of water without chlorophyll) is used to calculate a daily k (total extinction coefficient of water) based on the phytoplankton compartment size. This k then is used in the variable light equation (see above).

Nutrient limitation has been addressed in the model by using a Michaelis-Menten type equation:

$$\frac{r}{r_{max}} = \left[\frac{n}{k_s + n}\right]$$

where r = realized growth rates

n = the concentration of the nutrient being considered

k_s = the concentration of the nutrient at which growth is ½ the maximum.

This type of equation is widely used in phytoplankton nutrient relationships (Eppley and Strickland 1968, Steel and Frost 1977, DiToro 1980). The equation describes the increase in growth as the concentration of nutrient increases from much smaller to much larger than k_s.

Nitrogen is the nutrient currently included in the Patuxent estuary simulation, since the P:N input values seem to indicate the limiting roles of the nutrient (Heinle et al. in press, Mihursky and Boynton 1978). CBEM has the capability, however, to test for the nutrient most limiting to phytoplankton growth (either N or P) and use it to reduce the maximum growth rate.

The instantaneous rate of phytoplankton growth, r_{max} is reduced by multiplying r_{max} by the nutrient and light equations:

$$r = r_{max}\left[\frac{n}{k_x + n}\right] \cdot \left[\frac{eF}{KZ}\right]\left[e^{\frac{-I}{I_{opt}}e^{-KZ}} - e^{\frac{-I}{I_{opt}}}\right]$$

which can be integrated over the depth of the water column.

Copepods: The copepods in the lower Patuxent estuary are dominated by Acartia tonsa and A. Clausi. A. tonsa is most abundant in the summer and A. clausi in the late winter, but A. tonsa is

found throughout the year (Heinle 1974). Rates of ingestion, respiration, and to a certain extent reproduction are controlled by temperature in the model. The copepod ingestion rate is calculated as a function of the rate of water filtered and the concentration of food in that water. However, since copepod feeding rates are dependent upon the concentration of food (Lamm and Frost 1976) a Michaelis-Menten type equation has been added (DiToro 1971). The filtration rates for the two species of Acartia are based on temperature. The following equations were calculated from published data (Anraku 1964) and are similar to the final equations used in CBEM; although slight adjustments were found to be necessary during calibration:

- Acartia tonsa

$$Fm = 0.053\ e^{0.15T}$$

- Acartia clausi

$$Fm = 0.076\ e^{0.13T} \qquad T \leq 15^{\circ}C$$

$$Fm = 0.534 \qquad T > 15^{\circ}C$$

where Fm = maximum filtering rate (liters per calorie of copepod per day)

e = base of natural logarithms

T = temperature $^{\circ}C$

The above equations calculate the maximum filtering rate at that temperature. This rate is then reduced by the following equation:

$$F = Fm \left[1 - \frac{P}{k_s + P} \right]$$

where F = realized filtering rate (liters per calorie of copepod per day

Fm = maximum filtering rate (liters per calorie of copepod per day

P = phytoplankton concentration (calories per liter)

k_s = phytoplankton concentration at which the filtration rate is ½ the maximum (calories per liter)

The amount of phytoplankton filtered per calorie of copepod per day is then calculated by multiplying the realized filtering rate by the concentration of phytoplankton.

Basic respiration rates of Acartia tonsa and A. clausi were also calculated from Anraku (1964). The respiration rates are, of course, dependent upon Q_{10} (physiological) values which can change depending upon various ecosystem parameters. Respiration rate equations may be adjusted in the model.

- Acartia tonsa

$$\frac{\text{calories respired}}{\text{calorie of copepod}} \text{ per day} = \begin{cases} 0.06e^{0.06T} & \text{when } T \leq 15°C \\ 0.02e^{0.02e^{0.09T}} & \text{when } T > 15°C \end{cases}$$

- Acartia clausi

$$\frac{\text{calories respired}}{\text{calorie of copepod}} \text{ per day} = 0.011e^{0.11T}$$

Copepod reproduction is the difference between assimilation and respiration (Petrusewicz 1967). This energy is stored first as eggs, then as juveniles, until a temperature determined development time has elapsed, at which time they enter the adult compartment. Reproduction for Acartia clausi is programmed to occur between 4 - 20°C, while A. tonsa has a lower limit to reproduction of 10°C (Jeffries 1962). These values reflect in general the temperature division between these two species.

Hatching times for the eggs of both species are based on the following equation (McLaren 1966, Nixon and Kremer 1978).

$$H_{days} = 12.0\ e^{-0.11T}$$

In the model, both Acartia tonsa and A. clausi follow this equation, which was calculated from a number of species. At the time of hatching approximately half of the egg weight becomes nauplii weight (Landry 1975). The juveniles enter a development array

where the projected development time, based on temperature, is calculated for each daily cohort. Equations for development were calculated from Heinle (1966), Miller et al. (1977), and Landry (1975).

The development of juveniles from nauplii to adults, encompasses a total weight gain of approximately 6μg (Heinle 1966, Miller et al. 1977). Since more than 75% of the weight gain by developing juveniles occurs in the last 25% of the development time (Miller et al. 1977), an equation relating development stage to weight has been calculated. Thus the juveniles gain a certain amount of weight each day. This increase in weight, plus a calculated respiration rate (based on temperature) is the juvenile assimilation. With an assimilation efficiency of 80% (Petipa 1978), the ingestion of the juveniles can be calculated and subsequently subtracted from the phytoplankton compartment.

Eggs and juveniles are reduced by a forced mortality rate in the model so that only a small percentage (less than 5%) of the original juveniles are alive to become adults. Mortality is calculated daily. In addition, the juvenile copepods are grazed by the adult copepods in direct proportion to the daily ratio of juveniles to phytoplankton. This ration is usually insignificant except when the phytoplankton compartment becomes small.

Ctenophores: The ctenophore Mnemiopsis leidyi is one of the primary zooplankton carnivores in the Chesapeake Bay (Miller 1974), as well as in other estuaries (Kremer 1979). In the Chesapeake Bay, Mnemiopsis is present in low abundance in the winter and early spring, but increases greatly in the summer (Miller and Williams 1972).

In the model, ingestion by Mnemiopsis is based upon the amount of water filtered. This is a temperature based function, intially calculated from Kremer (1979):

$$\left[\frac{\text{liters filtered}}{\text{calorie of ctenophor}}\right] \text{ per day} = 0.08\, e^{0.51T}$$

Unlike the copepods, the ingestion rate of Mnemiopsis increases with increasing concentrations of prey (Kremer 1979) so that the ingestion rate is calculated by multiplying the filtering rate by the concentration of prey.

Basic respiration rates of Mnemiopsis were calculated from Kremer (1978):

$$\frac{\text{calories respired}}{\text{calorie of ctenophore}} \text{ per day} = 0.0068\, e^{0.125\,T}$$

Benthic compartment: The model, at this time, essentially simulates the water column above an oyster (Crassostrea virginica) community. Three different levels of oyster density are used, depending on the substrate type (Dexter Haven, personal communication):

Rock bottom - 500 bushels/acre - 49 oysters/m^2

Sand/Shell bottom - 200 bushels/acre - 20 oysters/m^2

Mud/Shell bottom - 78 bushels/acre - 8 oysters/m^2

In the model, oysters remove phytoplankton from the water column at a rate proportional to the pumping rate. Although the size of the phytoplankton cells available will influence the amount removed from the water column (Haven and Morales-Alamo 1967), a generalized phytoplankton compartment renders such a differentiation unnecessary.

The pumping rate used in the model is the average rate of 6.3 l/hr per gram dry weight of oyster reported by Langefoss and Maurer (1975). Complete clearing of the pumped water by the oysters is assumed, but since the oysters function in the model is to graze the phytoplankton and supply bursts of meroplankton, no partitioning of the filtered material is necessary. Pumping by the oyster requires a temperature threshhold of 8°C (Galtsoff 1964), above which maximum pumping begins.

Above a temperature threshhold of 20 C oyster reproduction begins (Galtsoff 1964). This seasonal input into the plankton may have significant effects on planktonic relationships. Rates of oyster reproduction, larval biomass and metabolic functions are taken from the literature (Dame 1967, Galtsoff 1964, Rodhouse 1979, Grant and Olney 1979).

Other carnivorous zooplankton: Fish larvae can be significant predators on the zooplankton in Chesapeake Bay due to their abundance and residence time in the Bay. Larval stages of hogchoker (Trinectes maculatus), spot (Leiostomus xanthurus), croaker (Micropogon undulatus), and post larvae of menhaden (Brevoortia tyrannus) are common in the Bay at certain times of the year. Fish larvae are assigned a daily ingestion rate calculated as a percentage of the dry weight. A temperature relation was calculated to increase the daily ingestion rate to a maximum of 50% of the dry weight at maximum temperatures encountered (Laurence 1975). Larval fish become most important in the lower salinity reaches of the Bay tributaries.

Although Mnemiopsis leidyi is probably the major carnivorous zooplankter in the Bay (see above), two other zooplankters could be important predators. Beroe ovata, a ctenophore, and Chrysaora quinquecirrha, a coelenterate, feed upon Mnemiopsis as well as other organisms (Cargo and Shultz 1967). There is evidence that B. ovata which feeds heavily on Mnemiopsis and other ctenophores (Swanberg 1974) can decimate populations of Mnemiopsis (Kremer and Nixon 1976). For the most part, information is lacking on these two species, although several biomass and feeding reports have enabled us to use these organisms as a possible drain on Mnemiopsis leidyi and the copepods (Kremer and Nixon 1976, Miller 1974, Swanberg 1974).

Menhaden (Brevoortia tyrannus): Adult (but sexually immature) and juvenile (up to one year old) menhaden are extremely numerous in the Chesapeake Bay, supporting a large fishery in the Virginia portion (Bell and Fitzgibbon 1978, Frye 1979). Although menhaden have long been assumed to feed to a large degree on phytoplankton, recent evidence points toward a more zooplankton-oriented diet, especially where the phytoplankton is predominantly smaller than 15μ (Durbin and Durbin 1975). Feeding dominated by zooplankton prey may also be true in the Chesapeake Bay, where up to 80% of the phytoplankton have been reported to be less than 10μ in diameter (Van Valkenburg et al. 1978). Although biomass values for menhaden in the Chesapeake Bay are few, Durbin (1976) has given biomass values and metabolic relationship for menhaden in Narragansett Bay. Carter (personal communication) has taken biomass values in the Choptank River, Maryland. In the Chesapeake Bay model, menhaden can act as a forced drain on either the zooplankton or the phytoplankton, or both, and the impact of such a drain investigated. The form and intensity of possible menhaden drains were tested as shown in section 6, but were generally found to be realistic in the 5-10% range.

4. Computer Model - Program Structure

CBEM is programmed in Fortran V for use on the UNIVAC 1108 system (see above). The main program and approximately 21 sub-routines comprise CBEM. The main program coordinates the linear flow of the simulation by calling the appropriate subroutines. Subroutines fall into four general categories:

1. Input oriented subroutines
2. Internal subroutines
3. Output oriented subroutines
4. Salinity oriented subroutines

Functions not calculated in the subroutines (i.e. phytoplankton biomass) are calculated in the main program.

The following lists names and describes the primary subroutines in CBEM:

1) Input oriented subroutines

- CSOLAR - calculates the daily input of solar radiation (calories per square meter per day).
- CTEMP - calculates the daily water temperature.
- DATA - contains the input data needed to run the program. Initial compartment values, Michaelis - Menten constants, the length of time the program is to simulate, and other values are contained here. Coded instruction for various output formats, such as graphs, are also included in this subroutine.
- FOTO - the maximum phytoplankton growth rate, r_{max}, is calculated, as are the limiting values based on nutrients and light. r, the realized growth rate (before predation) is calculated in the product of these three values.
- MONTH, SEASON - these two subroutines locate the simulation output in useful time frames.

2) Internal Subroutines

- CALCMX - calculates the basic matrix from which the differential equations are calculated.
- DEGJUV - the initial amounts of time left as copepod eggs and juveniles are calculated.
- DELAY - calculates the daily hatching and growth rates of copepod eggs and juveniles, and mortality rates, including predation by adults.
- DEPROD - calculates the total weight gain of copepod juveniles and reduces the phytoplankton by an amount proportional to this gain.
- FUNC - creates the differential equations from the program matrix.
- NUTRNT - the nutrient compartments are increased and decreased in this subroutine.

3) Output oriented subroutines

- GRAPH - graphs the requested statistics.
- PRTDIF - the differential equations are printed.
- PRSTAT - the requested block of statistics are printed

4) Salinity oriented subroutines

- SALINE - contains the basic changes applied when salinity scenarios are shifted. Species presence, predation, respiration and other factors change with salinity.

5. Model Ouput

The basic simulation period of CBEM currently being used is one year. Compartment values can be printed daily, or any number of days may be omitted from the printout. Generally one day and five day increment printouts proved most useful in model development.

Three printout "packages" are basic to the model and provide most of the information required to understand the simulation. The first printout contains the standing crop (cal/m^3) of the interactive compartments and their ingestion and respiration rates. The month, day, and water temperature are also listed in this printout, as are the values for nutrients and the realized phytoplankton growth rate. An example of this printout format is shown in Table VI- 1.

The second printout package is useful in analyzing the results of a simulation. The two limiting values (see p.277) calculated from nutrients and light are listed in this printout, as are the values for the extinction coefficient of the water column, the depth of the euphotic zone, daily insolation, chlorophyll a, and the ratio of daily insolation to optimum insolation. The month and day are also listed in this printout, as is the maximum rate of phytoplankton growth (calculated from temperature) (Kremer and Nixon 1978).

The third printout format lists the productivities (cal/day) of the phytoplankton, copepods, and ctenophores, along with the basic standing crop information for those compartments. An example of this printout format is shown in Table VI- 2 .

Most of the above data can be output in graphical format, at any interval desired. Graphs, of course, show patterns that might be difficult to observe in standard numerical printouts. (Examples of graphical model output are shown in subsection 6.)

Initial conditions have been defined by utilizing the best possible values of winter data (on or about Dec. 15) in the literature on standing crop for each organism. In some cases this data is corrected seasonally, as when a predator is known to enter the estuary in the spring (and may not be present in winter; i.e. Chrysaeora). The data come from a wide variety of sources which have been discussed in Chapter III, many of which are cited in this chapter. Complete documentation on any particular species is available from WESTECH; however, the prime sources for the species modeling include:

- phytoplankton - Heinle 1974, Mackiernan (unpubl. data)
- Acartia spp. - Heinle 1966, Stross and Stottlemeyer 1965
- Ctenophore - Mihursky and Boynton 1978, Kremer and Nixon 1968
- predators - Cargo and Shultz 1967, Durbin and Durbin 1975, Homer and Boynton 1978, Miller 1974, Swanberg 1974

Physical data was derived from actual solar measurements in the Bay area (Cinquemani et al. 1978) as are temperature measurements (Ritchie and Genys 1975). Nutrient data was derived from USGS files and Mihursky and Boynton 1978.

In many cases, species feeding, respiration or other parameters were not known exactly for the Patuxent estuary. In other cases, data existed, but across some range of values. The model was calibrated by selecting and running CBEM with various biologically realistic values within such ranges of values, or through making biologically defensible judgements for minor alterations in values. Such judgements were based on other data whenever possible. For instance, phytoplankton growth temperature dependence was determined in some cases by using analysis of Chesapeake Bay chlorophyll data to correct productivity calculations originally made on Narraganset Bay (Kremer and Nixon 1978). The most biologically realistic runs were then selected to provide the calibrated values.

TABLE VI-1 Standard CBEM Printout

MTH	DAY	PHYTO	TURSA	CLAUST	CTEN	NUTRIENTS	TO IR	TO RS	T JUV	CL IO	CL RS	C JUV	CT IO	CT CL	CT RS	G	TEMP
DEC	1	3346.5	100.0	26.4	9.4	65000.0	.1529	-.1070	.0	.2402	-.0513	.2	.0179	.0034	-.0147	.0887	9.6
DEC	6	3996.8	100.3	28.9	7.4	51392.3	.1363	-.1009	2.8	.2616	-.0205	6.9	.0119	.0034	-.0136	-.0184	8.7
DEC	11	3430.1	101.8	34.2	5.8	12685.9	.1066	-.0954	3.6	.1140	-.0257	8.2	.0113	.0030	-.0126	.0797	7.7
DEC	16	4379.0	104.4	40.7	4.6	6167.3	.0933	-.0905	4.2	.1107	-.0234	9.0	.0108	.0042	-.0118	.0574	6.9
DEC	21	4865.2	108.0	47.8	3.6	4186.0	.0883	-.0863	6.4	.1022	-.0214	13.0	.0105	.0046	-.0110	.0226	6.1
DEC	26	5138.0	113.7	58.5	2.9	3072.9	.0762	-.0826	1.0	.0936	-.0198	7.5	.0104	.0053	-.0104	.0145	5.3
DEC	31	5284.5	119.6	63.8	2.5	2408.5	.0699	-.0796	.0	.0862	-.0185	9.0	.0056	.0056	-.0099	.0098	4.7
JAN	36	5343.6	104.5	71.7	1.9	1849.2	.0654	-.0772	.0	.0801	-.0174	6.7	.0087	.0060	-.0095	.0066	4.2
JAN	41	5347.8	96.9	77.4	1.5	1410.6	.0597	-.0753	.0	.0755	-.0167	4.7	.0078	.0063	-.0092	.0045	3.8
JAN	46	5316.8	88.7	80.5	1.2	1114.1	.0555	-.0742	.0	.0725	-.0162	5.0	.0070	.0064	-.0090	.0033	3.5
JAN	51	5267.9	80.6	84.0	1.0	1974.2	.0542	-.0736	.0	.0710	-.0160	4.4	.0063	.0068	-.0089	.0057	3.4
JAN	56	5285.6	75.0	86.7	1.0	1814.8	.0526	-.0730	.0	.0697	-.0159	4.5	.0057	.0067	-.0088	.0051	3.3
JAN	61	5296.0	66.0	90.0	1.0	1795.0	.0524	-.0730	.0	.0697	-.0158	4.0	.0051	.0070	-.0088	.0052	3.3
FEB	66	5315.0	59.6	93.3	1.0	1612.6	.0512	-.0723	.0	.0681	-.0155	2.7	.0046	.0072	-.0087	.0045	3.1
FEB	71	5305.9	53.4	95.2	1.0	1315.0	.0486	-.0711	.0	.0654	-.0150	2.5	.0040	.0072	-.0085	.0033	2.8
FEB	76	5284.5	47.6	97.0	1.0	1207.8	.0477	-.0708	.0	.0645	-.0149	.6	.0036	.0073	-.0085	.0030	2.8
FEB	81	5264.7	42.4	98.3	1.0	1276.2	.0484	-.0711	.0	.0651	-.0150	.0	.0032	.0074	-.0085	.0035	2.8
FEB	86	5273.6	37.9	98.3	1.0	1506.5	.0506	-.0721	.0	.0674	-.0154	.0	.0029	.0075	-.0087	.0049	3.1
MAR	91	5320.8	34.2	98.2	1.0	1884.4	.0546	-.0737	.0	.0714	-.0160	.0	.0027	.0077	-.0089	.0068	3.4
MAR	96	5433.0	31.3	98.2	1.0	2396.1	.0605	-.0759	.0	.0774	-.0169	.0	.0026	.0080	-.0093	.0106	3.9
MAR	101	5675.7	29.2	98.2	1.0	1029.1	.0691	-.0788	.0	.0859	-.0181	.0	.0025	.0084	-.0098	.0060	4.5
MAR	106	5786.9	28.2	98.1	1.0	1771.9	.0798	-.0822	.0	.0959	-.0196	.1	.0026	.0089	-.0105	.0127	5.2
MAR	111	6116.8	28.1	98.1	1.0	2614.8	.0947	-.0862	.0	.1098	-.0214	.6	.0027	.0095	-.0110	.0219	6.0
MAR	116	6785.4	28.1	98.0	1.0	3543.5	.1157	-.0908	.0	.1287	-.0235	1.4	.0029	.0101	-.0116	.0333	6.9
MAR	121	7973.9	28.1	98.0	1.0	4546.9	.1440	-.0960	.0	.1543	-.0260	2.4	.0031	.0109	-.0127	.0456	7.8
APR	126	9170.7	28.1	97.9	1.0	5616.2	.1539	-.1018	.0	.2933	-.0292	3.5	.0034	.0118	-.0156	-.0975	8.8
APR	131	2867.8	25.3	97.9	1.0	8986.5	.1480	-.1085	.1	.2688	-.0325	5.9	.0035	.0125	-.0149	-.1387	9.8
APR	136	1659.6	13.8	98.8	1.0	19169.3	.1394	-.1154	.3	.2329	-.0365	9.1	.0020	.0140	-.0163	-.0109	10.9
APR	141	1693.2	7.4	100.1	1.0	28280.1	.1685	-.1231	.4	.2769	-.0411	11.1	.0011	.0155	-.0177	.0833	12.0
APR	146	2372.5	5.0	102.9	1.0	27659.8	.2528	-.1319	.6	.3945	-.0463	12.4	.0008	.0173	-.0194	.0937	13.1
APR	151	3125.0	5.2	110.1	1.0	20145.7	.3508	-.1404	.5	.2449	-.0523	10.5	.0010	.0202	-.0211	.0546	14.2
MAY	156	3660.1	5.5	94.9	1.0	16343.2	.5208	-.1480	.0	.0379	-.0590	7.3	.0011	.0190	-.0251	.0314	15.3
MAY	161	4083.3	5.5	46.3	1.0	14501.0	.6507	-.1480	.1	.0512	-.0604	10.9	.0012	.0181	-.0251	.0237	16.3
MAY	166	4555.6	5.5	26.3	1.0	14080.2	.7953	-.1480	.6	.0113	-.0746	3.0	.0013	.0053	-.0274	.0365	17.4
MAY	171	5041.0	5.7	10.1	1.0	14905.41	.0002	-.1480	1.5	.0043	-.0836	.0	.0015	.0096	-.0297	.0566	18.4
MAY	176	7549.0	7.3	3.1	1.0	15061.51	.2658	-.1480	2.0	.0017	-.0934	.0	.0020	.0089	-.0322	.0656	19.4
MAY	181	10236.7	9.7	1.0	1.0	16489.51	.8124	-.1480	3.5	.0007	-.1038	.0	.0029	.0083	-.0348	.0655	20.4
JUNE	186	13774.6	14.4	1.0	1.0	18036.62	.1970	-.1480	8.0	.0003	-.1149	.0	.0047	.0083	-.0374	.0653	21.3
JUNE	191	17348.2	23.5	1.0	1.0	19543.52	.5887	-.1480	29.0	.0001	-.1262	.0	.0081	.0083	-.0401	.0580	22.2
JUNE	196	19717.1	59.4	1.0	1.0	22457.92	.9711	-.1584	66.4	.0001	-.1380	.0	.0219	.0084	-.0426	.0769	23.0
JUNE	201	18608.4	119.0	1.0	1.0	26668.03	.3012	-.1694	121.8	.0000	-.1498	.0	.0466	.0084	-.0454	.1447	23.7
JUNE	206	8966.4	213.7	1.0	1.1	31508.93	.2282	-.1901	148.9	.0000	-.1615	.0	.0493	.0084	-.0480	.4060	24.4
JUNE	211	3628.2	286.2	1.0	1.4	63602.02	.6403	-.1904	101.5	.0000	-.1727	.0	.1868	.0084	-.0504	.9269	25.0
JULY	216	3350.0	294.4	1.0	1.5	77544.42	.8142	-.1999	133.2	.0000	-.1834	.0	.1332	.0085	-.0526	1.0582	25.5
JULY	221	2967.7	334.1	1.0	2.0	134928.02	.8415	-.2085	84.9	.0000	-.1930	.0	.1569	.0085	-.0546	1.3146	26.0
JULY	226	2577.4	352.5	1.0	2.8	207443.82	.8140	-.2159	93.3	.0000	-.2015	.0	.1707	.0085	-.0564	1.4902	26.4
JULY	231	2177.8	361.1	1.0	4.1	297736.52	.7148	-.2221	101.7	.0000	-.2085	.0	.1795	.0085	-.0578	1.6212	26.7
JULY	236	1929.9	368.9	1.0	6.3	497395.72	.6295	-.2267	87.2	.0000	-.2139	.0	.1839	.0085	-.0589	1.7024	27.0
JULY	241	1821.4	371.8	1.0	9.7	509269.42	.5847	-.2298	65.5	.0000	-.2174	.0	.1902	.0085	-.0596	1.7454	27.1
AUG	246	1771.1	373.2	1.0	15.0	624124.92	.5561	-.2312	52.3	.0000	-.2190	.0	.1919	.0085	-.0599	1.7596	27.2
AUG	251	1681.1	364.4	1.0	24.2	754724.22	.6449	-.2308	59.3	.0000	-.2186	.0	.1871	.0085	-.0598	1.7382	27.2
AUG	256	1953.4	352.8	1.0	37.0	848655.6	.6554	-.2286	75.4	.0000	-.2162	.0	.1798	.0085	-.0593	1.7044	27.1
AUG	261	2040.6	346.3	1.0	54.0	950857.9	.6404	-.2250	98.1	.0000	-.2128	.0	.1769	.0085	-.0585	1.6500	26.9
AUG	266	2658.1	323.3	1.0	79.2	1034549.1	.9482	-.2194	124.3	.0000	-.2089	.0	.1690	.0085	-.0575	1.5340	26.6
AUG	271	4061.5	276.4	1.0	102.8	1068765.0	.3605	-.2131	169.1	.0000	-.1964	.0	.1454	.0085	-.0557	1.3338	26.3
SEPT	276	7766.7	257.0	1.0	80.4	967355.43	.8536	-.2052	71.0	.0000	-.1833	.0	.1196	.0085	-.0539	1.0947	25.9
SEPT	281	13570.0	227.7	1.0	59.3	854215.14	.0249	-.1962	114.5	.0000	-.1793	.0	.1014	.0084	-.0518	.7128	25.4
SEPT	286	17461.8	211.8	1.0	40.0	93379.23	.8405	-.1864	24.0	.0000	-.1604	.0	.0502	.0084	-.0495	.3497	24.8
SEPT	291	5213.2	200.0	1.0	27.4	37532.72	.6659	-.1760	75.6	.0000	-.1570	.0	.0442	.0084	-.0470	.4490	24.2
SEPT	296	6090.2	211.1	1.0	17.1	34781.82	.5050	-.1652	34.3	.0000	-.1453	.0	.0444	.0084	-.0444	.3903	23.5
SEPT	301	5914.9	211.0	1.0	11.9	30097.7	.2209	-.1542	28.6	.0001	-.1353	.0	.0761	.0084	-.0410	.2640	22.7
OCT	306	5990.2	214.1	1.0	7.7	27722.	.9543	-.1430	21.1	.0001	-.1249	.0	.0725	.0085	-.0391	.2001	21.9
OCT	311	5790.5	215.9	1.0	5.0	26836.21	.7075	-.1480	19.6	.0008	-.1147	.0	.0680	.0085	-.0845	.1596	21.0
OCT	316	5602.2	218.7	1.0	3.2	26063.11	.4701	-.1480	15.3	.0008	-.1050	.0	.0640	.0083	-.0849	.1168	20.1
OCT	321	5427.9	221.0	1.0	2.1	25123.01	.0902	-.1480	10.8	.0840	-.0859	.0	.0599	-.0083	-.0818	.0769	19.1

TABLE VI-2 CBEM Printout with Productivity Calculations

MONTH	DAY	PHYTOPLANKTON	A. TONSA	A. CLAUSI	CTENOPHORES	NUTRIENTS	PROD. OF PHYTOPLANKTON	PROD. OF A. TONSA	PROD. OF A. CLAUSI	PROD. OF CTENOPHORES
DEC	1	3346.5	100.0	26.4	9.4	85000.0				
DEC	6	3996.8	100.3	28.9	7.4	81592.3	691.1	14.8	9.9	.1
DEC	11	3429.9	101.8	34.2	5.8	12686.3	315.4	11.0	5.4	.1
DEC	16	4378.0	104.4	40.7	4.6	6169.1	186.6	10.6	6.1	.1
DEC	21	4863.3	108.0	47.8	3.6	4188.3	120.4	9.7	6.7	.1
DEC	26	5134.9	113.7	58.5	2.9	3073.6	80.9	9.1	7.7	.0
DEC	31	5279.6	110.8	63.8	2.3	2409.7	56.3	7.9	7.4	.0
JAN	36	5336.0	104.5	71.7	1.9	1651.4	38.3	6.7	7.7	.0
JAN	41	5335.2	96.8	77.4	1.5	1415.4	26.0	5.8	7.8	.0
JAN	46	5297.3	88.6	81.6	1.2	1122.2	18.7	5.0	7.9	.0
JAN	51	5242.1	80.5	86.3	1.0	1985.0	15.4	4.4	8.1	.0
JAN	56	5252.3	72.9	89.8	1.0	1828.1	27.4	5.9	8.3	.0
JAN	61	5254.9	65.8	94.4	1.0	1812.0	27.1	5.5	8.7	.0
FEB	66	5265.9	59.4	98.6	1.0	1630.0	26.1	3.1	9.0	.0
FEB	71	5249.0	53.2	101.3	1.0	1333.5	18.6	2.6	8.8	.0
FEB	76	5221.0	47.4	104.6	1.0	1226.7	16.2	2.3	8.9	.0
FEB	81	5199.6	42.2	105.4	1.0	1295.1	17.7	2.0	9.1	.0
FEB	86	5198.8	37.7	105.3	1.0	1525.9	23.8	1.9	9.4	.0
MAR	91	5239.7	33.9	105.3	1.0	1904.5	33.0	1.8	9.9	.0
MAR	96	5345.0	31.0	105.3	1.0	2417.3	53.2	1.8	10.8	.0
MAR	101	5578.2	28.9	105.2	1.0	1051.5	86.9	1.9	12.0	.0
MAR	106	5681.7	27.8	105.2	1.0	1796.2	64.5	2.1	13.5	.0
MAR	111	5999.4	27.7	105.1	1.0	2642.1	121.2	2.5	15.6	.0
MAR	116	6650.8	27.7	105.1	1.0	3574.8	208.5	3.1	18.5	.0
MAR	121	7813.7	27.7	105.0	1.0	4583.4	341.7	4.0	22.7	.0
APR	126	9017.4	27.7	105.0	1.0	5659.4	330.7	4.5	40.2	.0
APR	131	2814.2	24.9	104.9	1.0	9233.2	310.6	3.8	32.5	.0
APR	136	1640.0	13.5	106.2	1.0	19608.8	389.3	1.8	25.7	.0
APR	141	1684.2	7.2	108.1	1.0	20899.9	578.5	1.1	30.1	.0
APR	146	2376.7	4.9	111.8	1.0	28182.1	897.1	1.1	48.4	.0
APR	151	3075.1	5.1	119.9	1.0	20674.3	1034.4	1.8	80.7	.0
MAY	156	3513.0	5.3	127.1	1.0	18862.6	1112.7	3.2	119.2	.0
MAY	161	3766.7	5.3	129.0	1.0	18356.3	1309.0	4.3	170.1	.0
MAY	166	4523.8	5.3	138.5	1.0	16160.2	1557.2	6.3	71.8	.0
MAY	171	5984.0	5.4	141.6	1.0	17301.3	2116.4	10.2	22.9	.0
MAY	176	8583.3	6.6	96.1	1.1	17534.6	2967.9	20.0	5.9	.0
MAY	181	11579.3	8.9	37.1	1.0	17562.0	3768.7	65.9	1.0	.0
JUNE	186	14837.9	13.5	11.0	1.0	18224.1	4803.8	155.5	.1	.0
JUNE	191	17984.7	22.3	3.0	1.0	19541.8	5752.5	460.8	.0	.0
JUNE	196	20082.4	57.0	1.0	1.0	22335.9	6738.6	1894.5	.0	.0
JUNE	201	18970.2	114.6	1.0	1.0	26442.1	7592.0	6348.2	.0	.0
JUNE	206	9557.3	207.1	1.0	1.1	31255.8	5745.2	13357.2	.0	.1
JUNE	211	3577.8	240.3	1.0	1.3	61726.3	4338.8	5801.5	.0	.1
JULY	216	3402.5	292.1	1.0	1.5	75976.0	4506.4	8968.4	.0	.2
JULY	221	3000.1	332.5	1.0	1.9	134555.8	4952.0	8908.6	.0	.3
JULY	226	2581.9	351.4	1.0	2.7	205775.2	4912.2	8196.5	.0	.5
JULY	231	2179.4	360.5	1.0	3.9	295976.0	4563.6	7907.4	.0	.7
JULY	236	1929.8	363.6	1.0	6.0	395621.9	4191.0	8052.3	.0	1.1
JULY	241	1819.0	371.9	1.0	9.2	507586.7	4112.1	6284.5	.0	1.7
AUG	246	1767.1	373.7	1.0	14.6	622597.3	3938.9	6840.5	.0	2.8
AUG	251	1859.4	369.9	1.0	14.1	736367.4	4102.3	6472.6	.0	2.7
AUG	256	1813.8	369.1	1.0	13.4	849380.6	3990.5	6853.5	.0	2.5
AUG	261	1890.0	373.0	1.0	12.7	960040.6	4090.4	6345.5	.0	2.4
AUG	266	2044.6	378.0	1.0	12.1	1067034.6	4193.4	6379.4	.0	2.3
AUG	271	2239.8	377.2	1.0	11.3	1163616.5	4427.6	6855.3	.0	2.1
SEPT	276	3413.7	384.3	1.0	7.0	1231277.0	6386.8	7302.5	.0	1.3
SEPT	281	5327.3	382.5	1.0	4.3	1187891.3	8359.0	15080.2	.0	.7

6. Agreement with Observed Data (Model Validation)

Although some of the basic data used to program the responses of organisms in CBEM comes from laboratory studies or studies on ecosystems other than the Chesapeake Bay, the physical parameters which drive and control the system must come from the system being modeled. The physical factors currently being utilized in the model are those from the lower Patuxent estuary. Whenever possible, biolgical data, such as seasonal standing crop, were taken from studies done in this river reach. When values were not available, such as for the seasonal abundance of the ctenophore Mnemiopsis leidyi, research conducted at other locations was used for data.

Similar constraints were present for the historical time period in which the data was taken. Ideally, the data used should be as current as possible to reflect the present state of the area being modeled. Even better, the modeling effort should be integrated into a research program in which the two approaches can complement each other and indicate the best directions for both the research and modeling. CBEM, however, has been developed to utilize the present knowledge of the Bay and is not associated with a research program. We have used data from a number of historical periods (in general different from that data used for calibration) to compare with the output from CBEM for purposes of model validation. Details of the results of several simulations are discussed below and compared with reported data.

Phytoplankton values, as simulated by the model, in general showed a good fit to published values (Figure VI-5). Winter and early spring values follow the observed values well, as does the spring-summer bloom. Summer values fall a little lower than the data might indicate but are still above the minimum observed values. In the early fall the model shows a large phytoplankton bloom that is not indicated in the observed data. This bloom is inherent in the simulation. Higher numbers

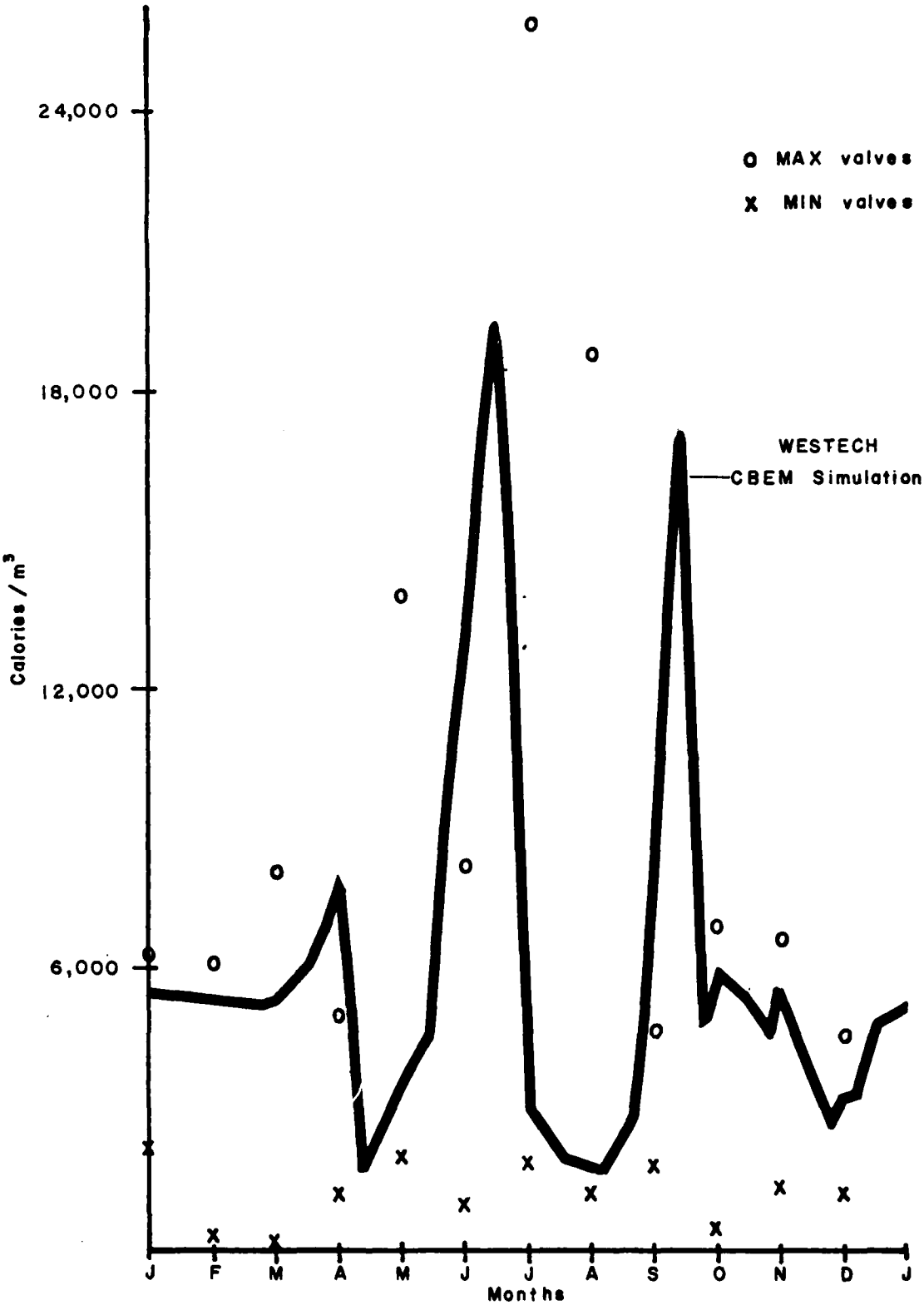


Figure VI-5 SIMULATED AND OBSERVED PHYTOPLANKTON ABUNDANCE

Sources of observed data: ANSP, unpub., 1975-79 ; Flemer et al, 1970 ; Stross and Stottlemyer, 1965

of copepod grazers shortens the duration of the bloom, and delays its onset, but the intensity of the phytoplankton growth is not depressed (see below). This aspect of the simulation is currently under study and may be due to inaccurate nutrient data, missing drains or other factors. After this bloom, however, phytoplankton levels agree very well with observed values.

CBEM simulations of copepod biomass compare favorably with the rather limited data available (Figure VI-6). Acartia tonsa values are low in the winter and decrease steadily through May, after which they increase rapidly. The summer peak of A. tonsa agrees well with the observed data. After abundant copepods in July and August there is a decrease beginning in September. The model simulation shows an elevated abundance of copepods midway through the fall decline, while the observed data shows the copepods to continue declining to low abundance. These higher levels of copepods in the fall reflect the interactions occurring between copepods and the fall bloom of phytoplankton previously discussed. A large amount of energy is flowing into the copepods at this time from the phytoplankton.

Data reported from a less saline reach of the Patuxent estuary (Heinle 1966) indicates a somewhat different pattern than that discussed above (Figure VI-7). Here A. tonsa (adults) show a peak abundance in March and then a slow, somewhat irregular decline to the end of May. There seems to be no winter decline, although overall abundance levels are lower. This is not unexpected, however, since in the less saline areas of the river A. tonsa is found with, and presumably competes with, Eurytemora affinis (Heinle and Flemer 1975).

Acartia clausi values from the CBEM simulations (Figure VI-7) were slightly higher than the limited observed data (Pans unpublished data - not shown). A. clausi is essentially gone from the Patuxent estuary by June, and this is reflected in the simulation run. Herman et al. (1968) found that A. clausi became increasingly dominant in comparison to A. tonsa from March to mid-May (Figure VI-8) and this is also reflected in the model simulation.

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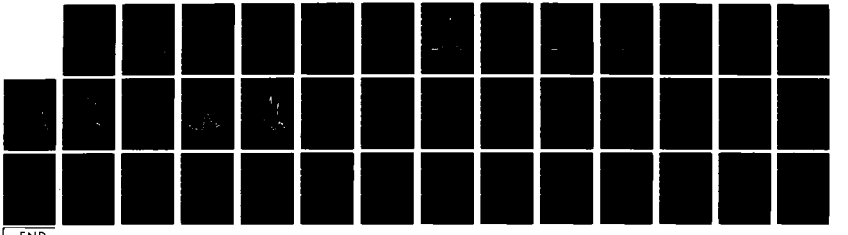

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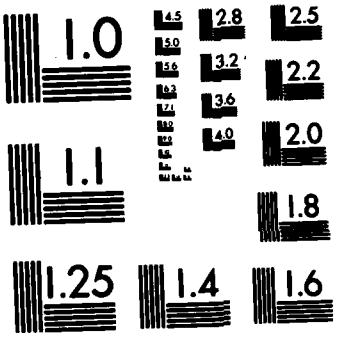

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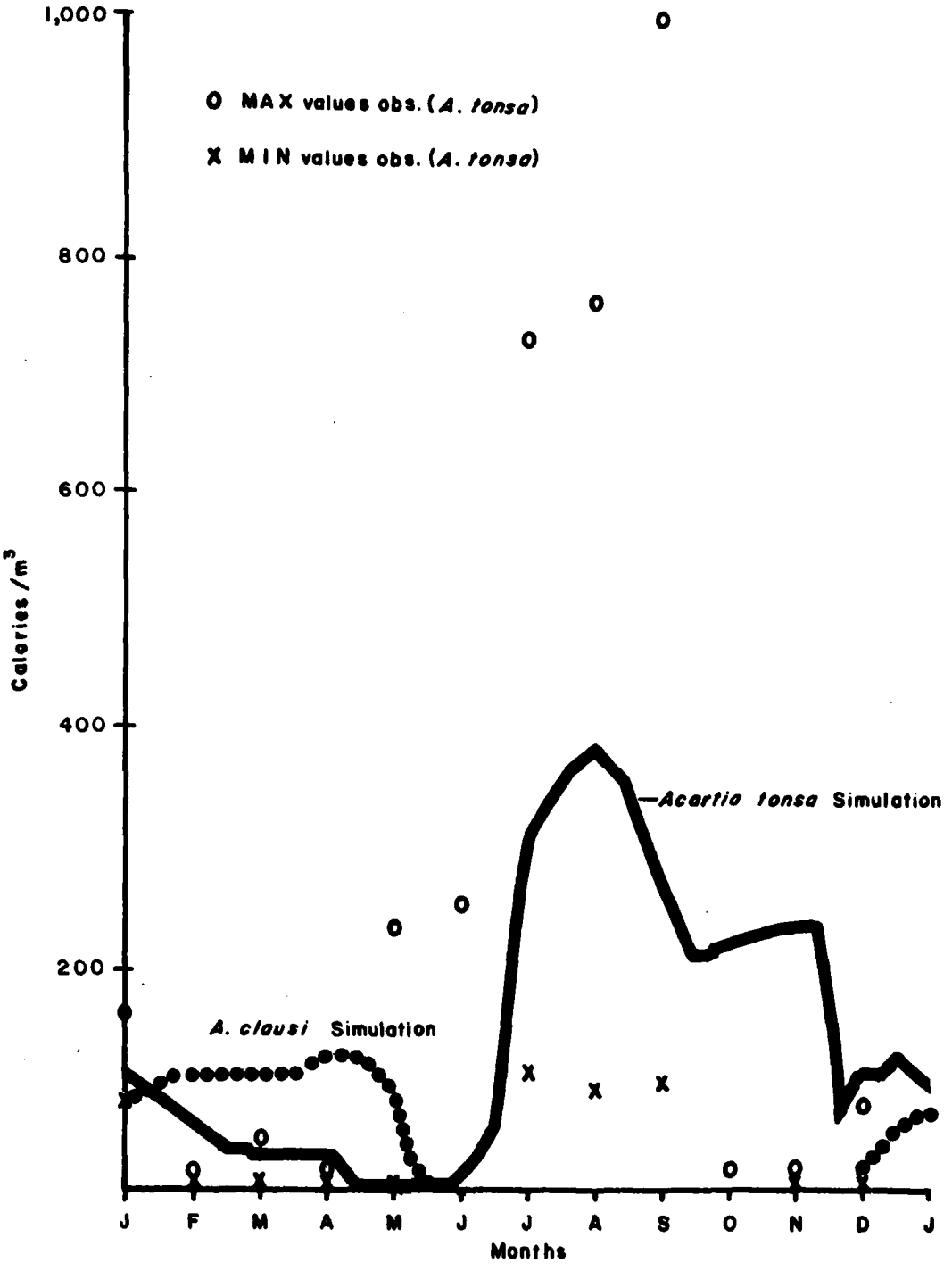

Figure VI-6 SIMULATED AND OBSERVED COPEPOD ABUNDANCE

Source of observed data : ANSP, 1975-77

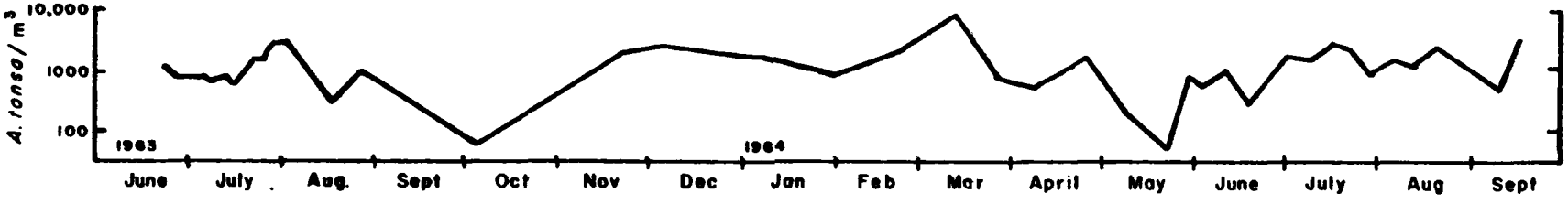

Figure VI-7

ABUNDANCE OF *Acartia tonsa* ADULTS IN THE PATUXENT ESTUARY

June 1963 - Sepetember, 1964

Source: Heinle, 1974

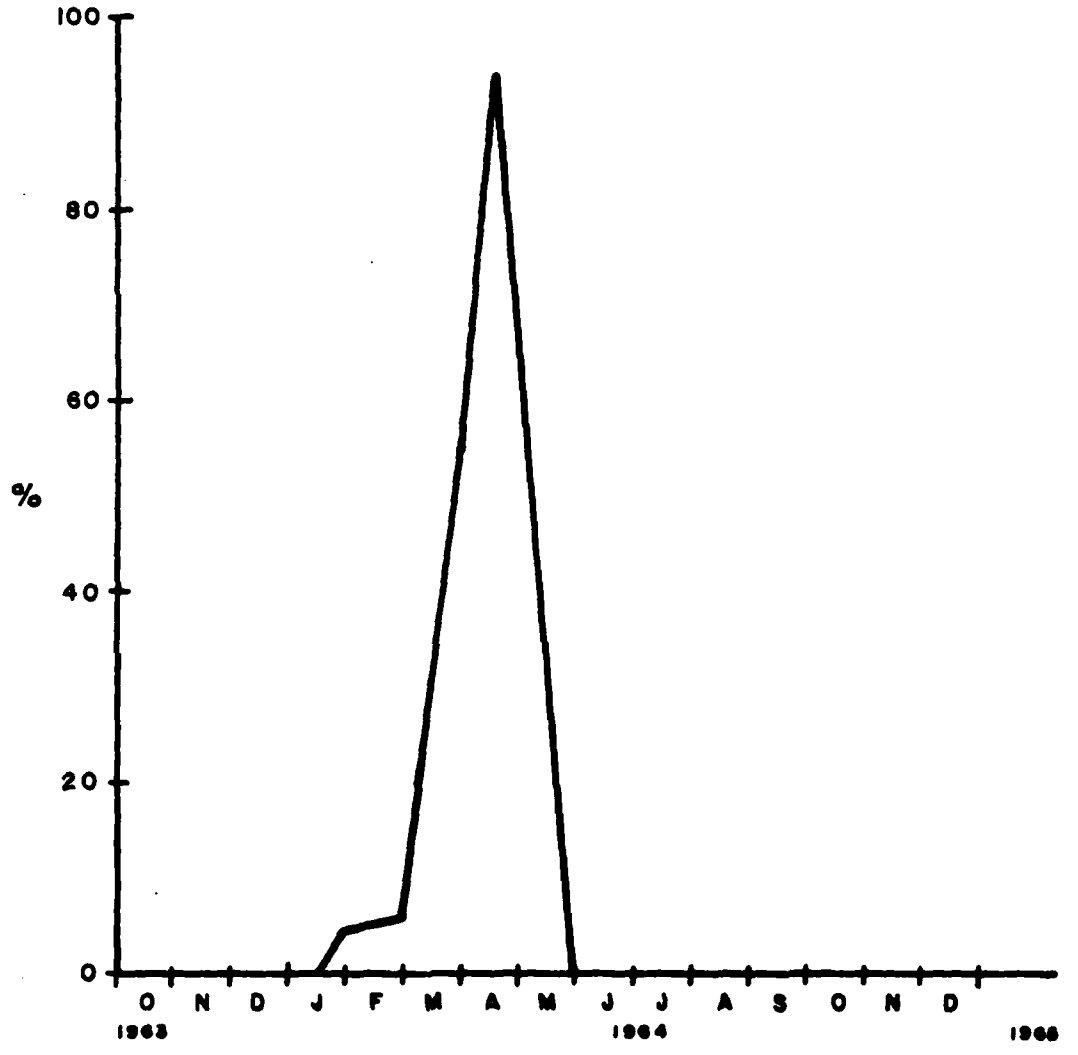

Figure VI- 8. PERCENT DISTRIBUTION OF *Acartia clausi* IN THE LOWER PATUENT ESTUARY (mile 10.8)*

Source: Herman et al., 1968

*maximum level set to 100%.

As previously stated, information on the abundance of Mnemiopsis leidyi in the Patuxent estuary is sparse. Information is available on the combined abundance of Mnemiopsis and Chrysaora quinquecirrha (Mihursky, McErlean and Herman 1967). Ziegenfuss and Cronin (1958, reported in Mihursky and Boynton 1978) reported an increase in ctenophore abundance beginning in early July and peaking in late summer. Peak densities for Solomons and Broomes Island were 9 and 32 individuals /m^3. This would correspond to volumes (#) of ctenophores of 261 and 928/m^3 respectively (Bishop 1967). These values are high compared to the peak of 33 /m^3 found in the York River (Burrell and Van Engel 1976) and a peak of about 50 /m^3 reported from Narragansett Bay (Kremer 1976). The maximum values found in Broomes Island samples by Mihursky McErlean and Herman (1967) for ctenophores and Chrysaora combined was 43 /m^3. The CBEM simulation peaked at 100 cal/m^3(21/m^3) (Figure VI-9). The model simulation show a rapid increase of this species. This explosive population growth is characteristic of Mnemiopsis (Kremer 1976).

The CBEM simulation of the lower Patuxent estuary is in general agreement with the observed data. The early fall simulations show a burst of energy going through the system which elevates the phytoplankton and copepod levels beyond expected levels. However, levels quickly fall to the range of observed data.

D. ALTERNATIVE SALINITY SCENARIOS

Several very preliminary simulations were done under a generalized scenario of "increased salanity" corresponding to changes of 2-5%. These included the addition of B. ovata, a ctenophore predator of Mnemiopsis. Although Beroe has been reported from the Patuxent estuary (Hermal et al. 1968), it does not occur there in appreciable numbers except during low flow periods. It is normally restricted to areas of higher salinity (Burrell 1972). Three levels of Beroe predation were simulated; 10$, 20% amd 50%. As a preliminary investigation into the effects of physiological changes associated with modified salinity regimes we altered the standard physiological response of A. clausi (Figure VI-10).

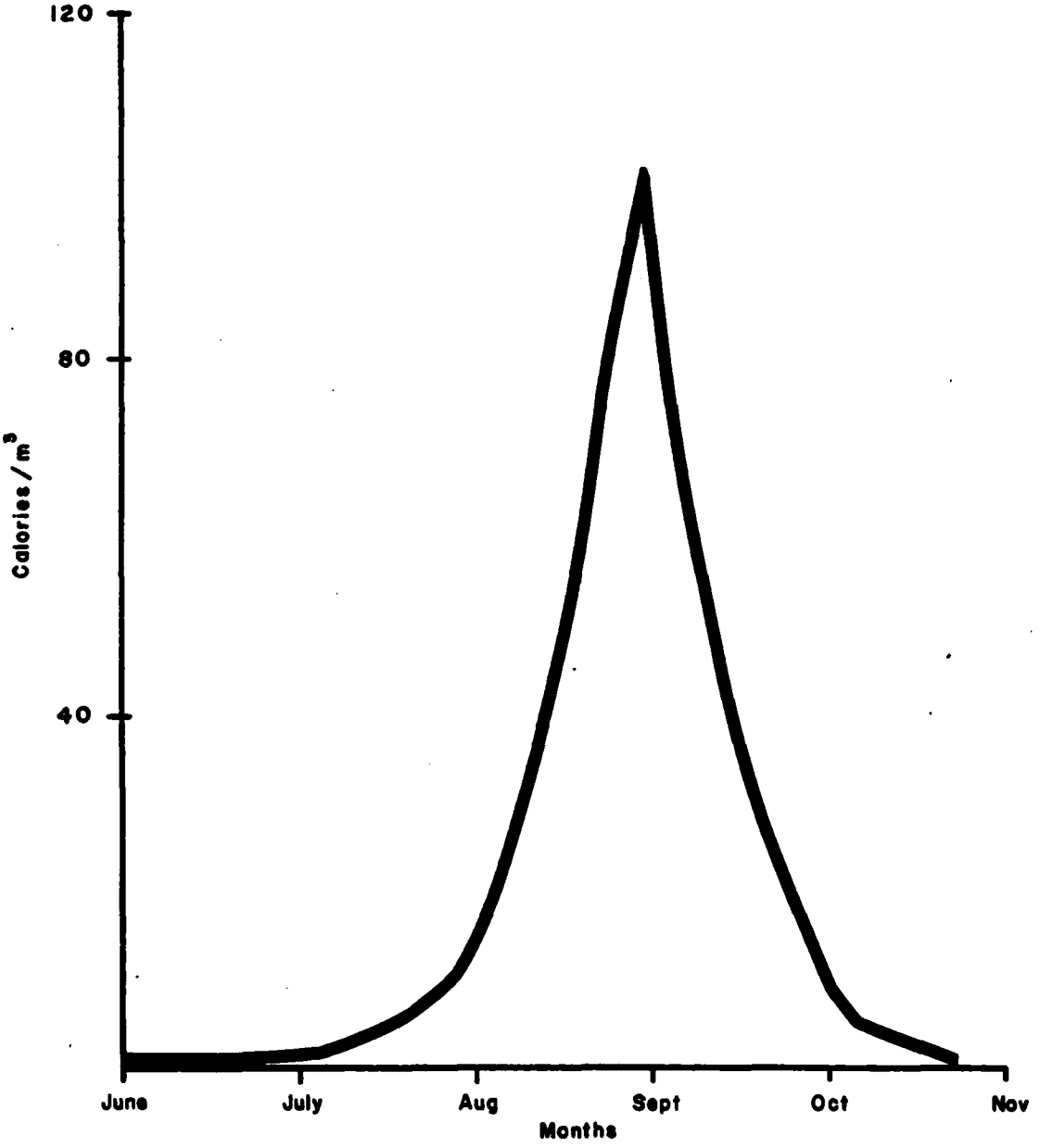

Figure VI-9 SIMULATED BIOMASS OF *Mnemiopsis leidyi*

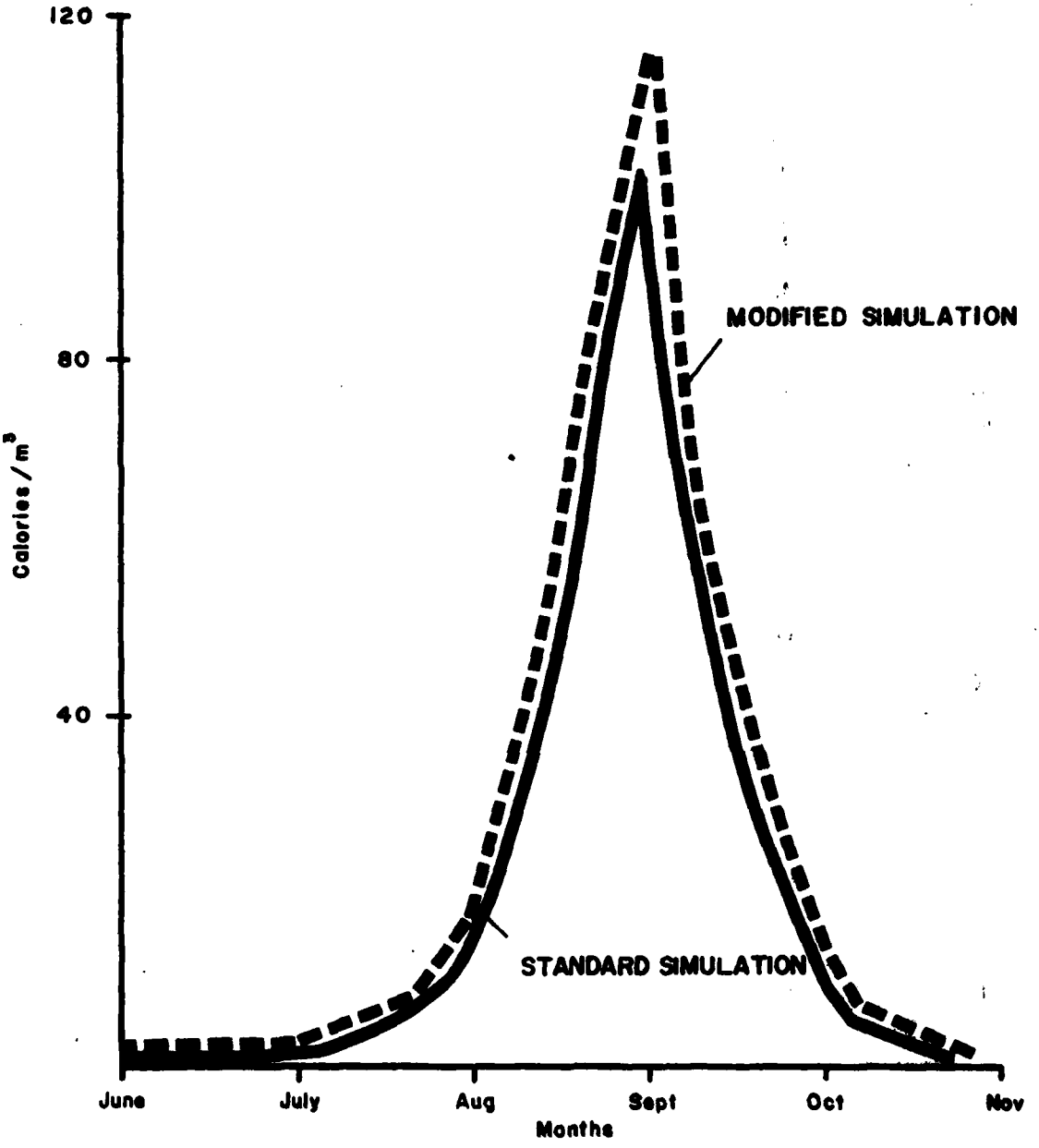

Figure VI-10 SIMULATED RESPONSE OF *Mnemiopsis leidyi* WHEN THE PHYSIOLOGICAL RESPONSE OF *Acartia clausi* IS ALTERED.

(Jeffries 1962). At higher salinities A. clausi can apparently compete with A. tonsa more successfully as the temperature increases. Since competition between developing stages of the two species might be most intensive (Conover 1956) adults and juveniles were considered in these preliminary simulations.

Adding Beroe as a predator of Mnemiopsis had several interesting results (FiguresVI-11-13). Beroe was programmed to enter the Patuxent estuary in August (day 246) and remain until the end of the year (day 365). A daily predation rate of 10% of Mnemiopsis had a pronounced effect reducing the peak biomass by approximately 80% (Figure VI-11). A daily predation rate of 20% by Beroe does not reduce the peak standing crop any further (because this now occurs before Beroe becomes a factor), but the decline in Mnemiopsis abundance is very rapid (Figure VI-12). At a predation rate of 50% the decline of Mnemiopsis is even more rapid (Figure VI-13). Such drastic reductions in Mnemiopsis abundance are known to occur in areas of overlap of these two species (Burrell and Van Engel 1976).

The effects of the reduced standing crop of Mnemiopsis on the copepod Acartia tonsa are immediately evident (Figure VI-14, VI-15). A. tonsa abundance is increased and the late summer copepod decline is delayed until November, a difference of about three months. There is little difference in A. tonsa biomass at the three levels of Beroe predation (the response to 50% predation is not shown). The other copepod in the model, Acartia clausi showed no change during this simulation because Beroe entered the run after A. clausi had declined.

The reduction of Mnemiopsis by Beroe had two effects on the phytoplankton. The fall bloom of phytoplankton was delayed several weeks, and the peak abundance of the bloom was reduced (Figure VI-16, VI-17). An interesting result is that the fall phytoplankton bloom is slightly larger in the run simulating a 20% predation rate than in the 10% predation run. This apparently resulted when the increased grazing released more nitrogen.

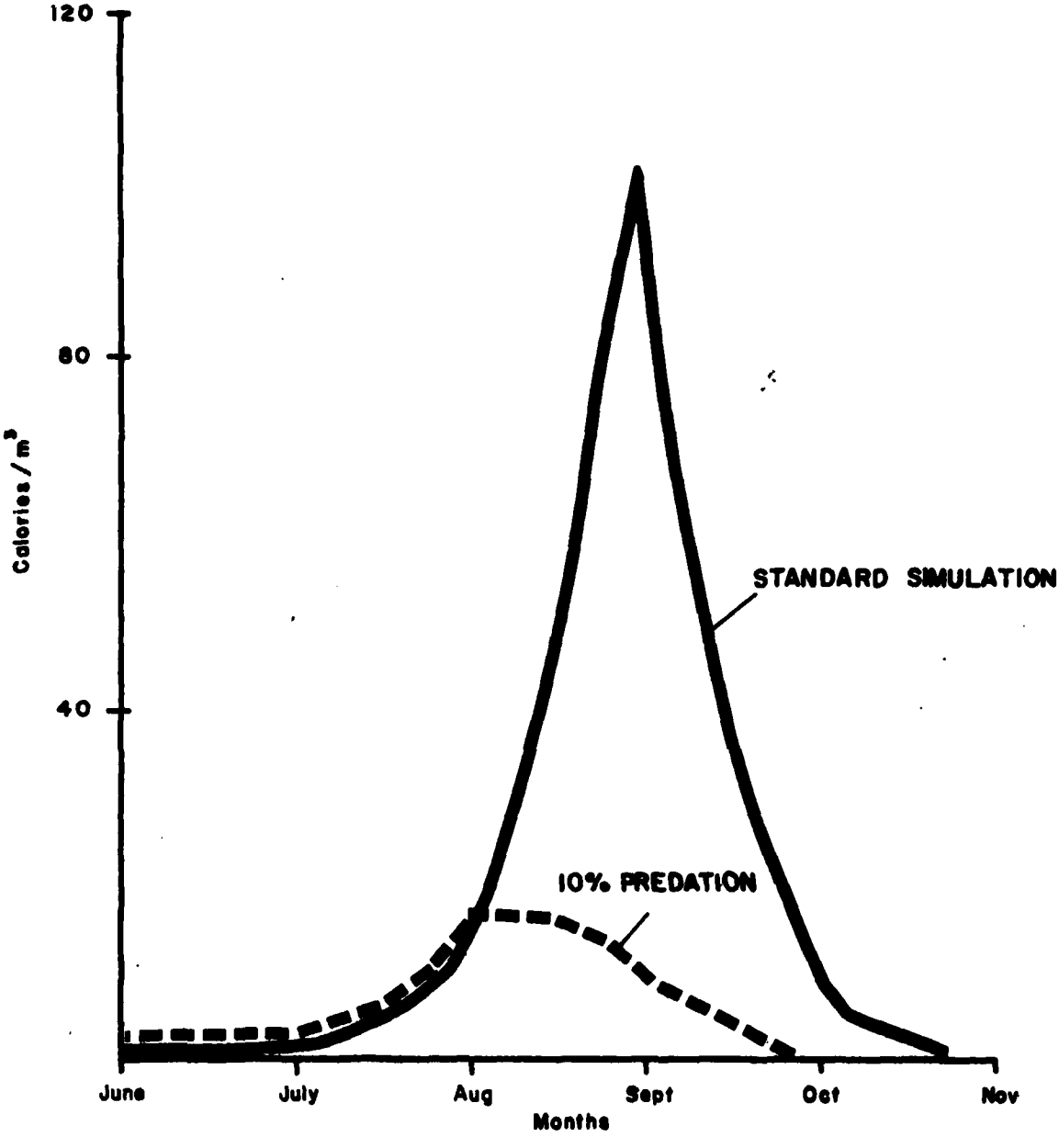

Figure VI - 11 SIMULATED ABUNDANCE OF *Mnemiopsis leidyi* PREDATED AT 10% DAILY.

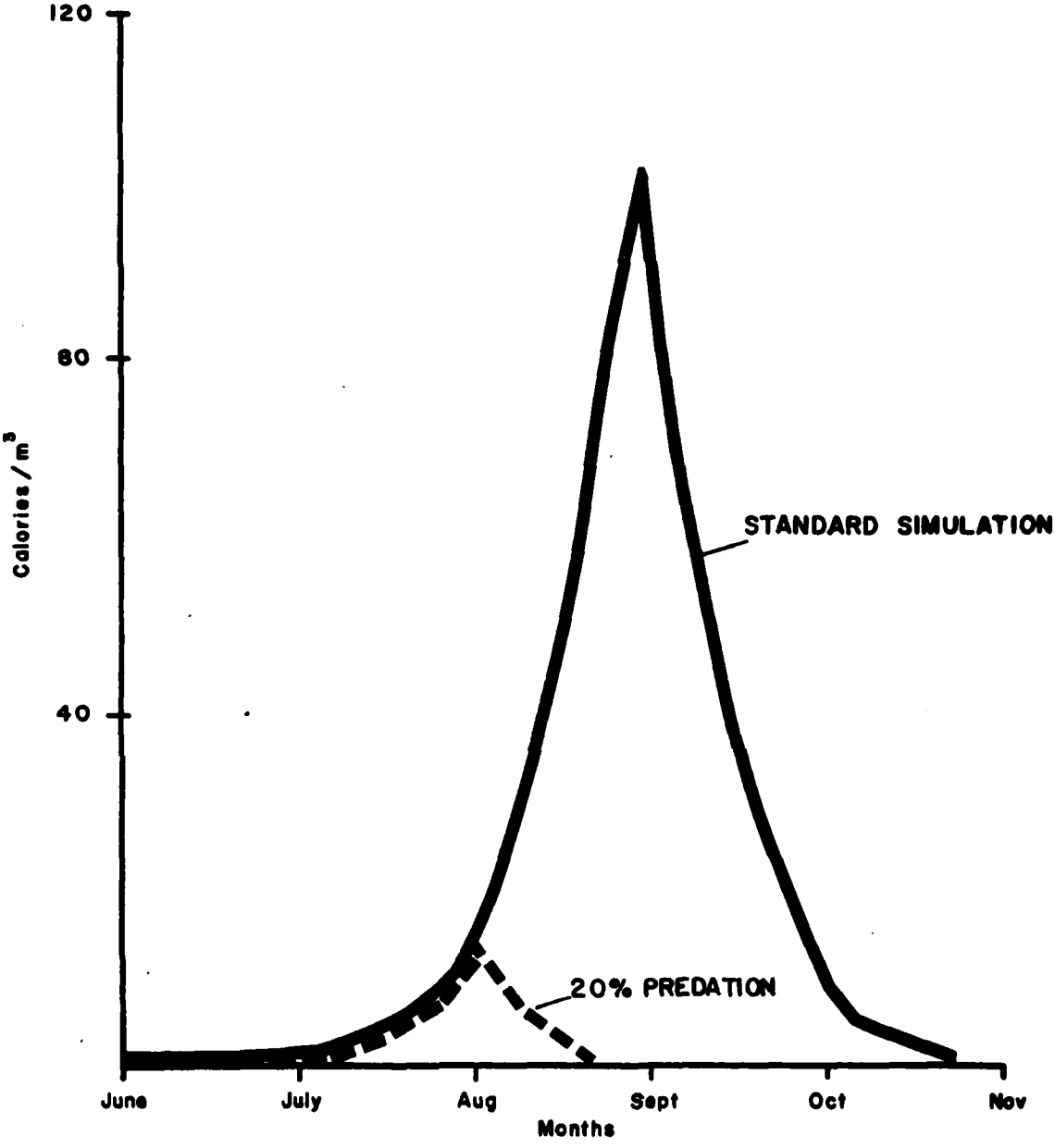

Figure VI - 12 SIMULATED ABUNDANCE OF *Mnemiopsis leidyi* PREDATED AT 20% DAILY.

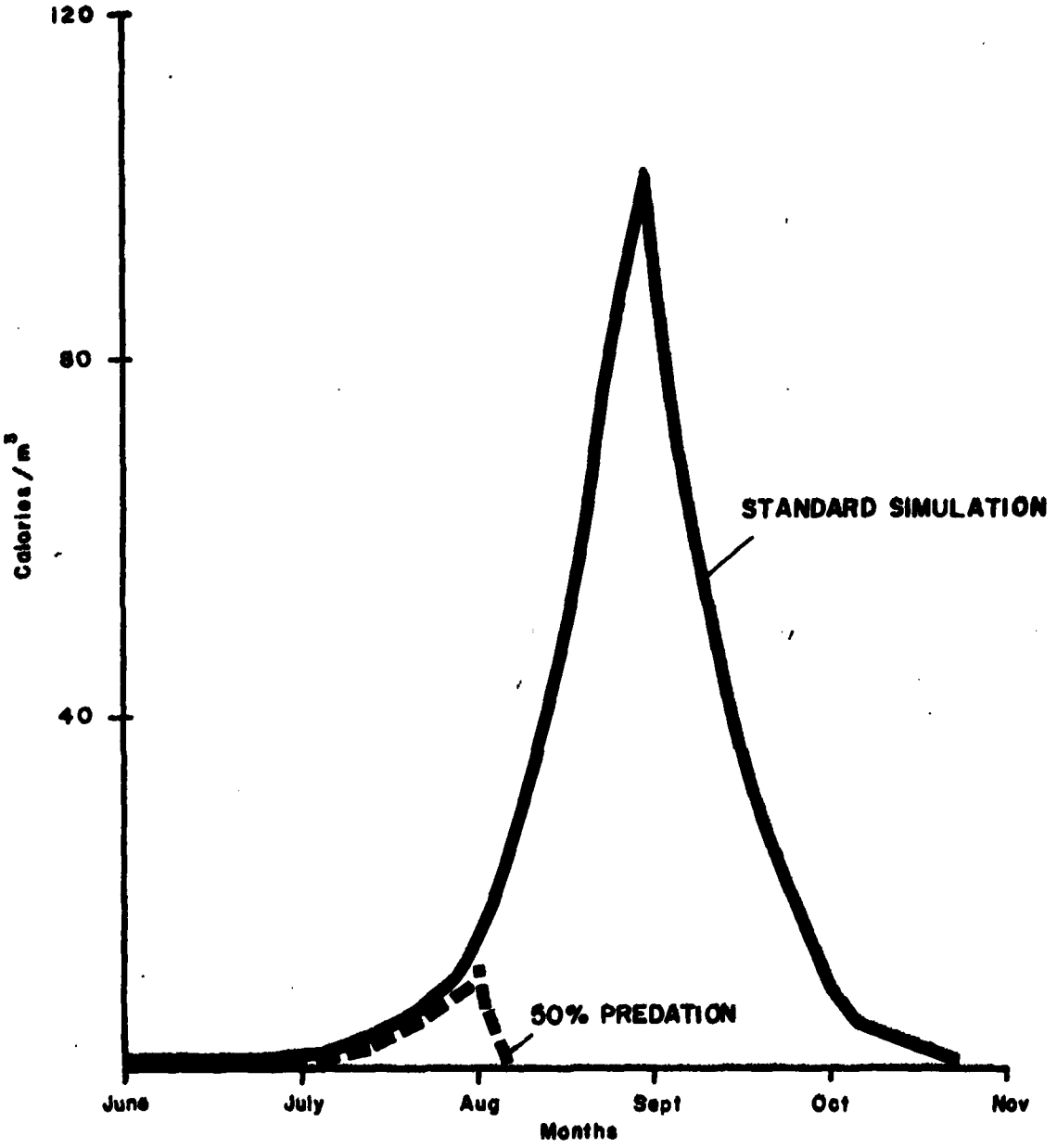

Figure VI 13 SIMULATED ABUNDANCE OF *Mnemiopsis leidyi* PREDATED AT 50% DAILY.

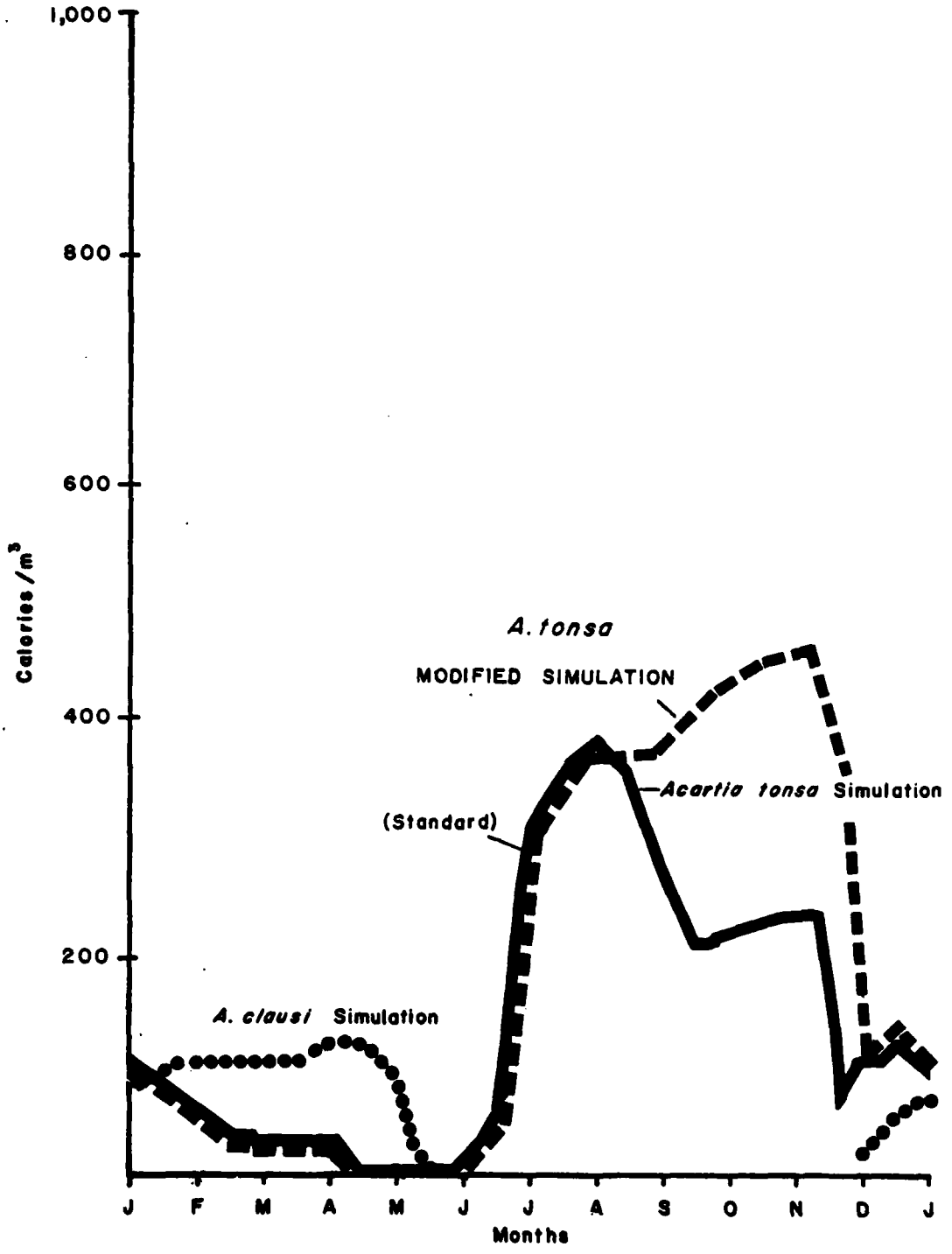

Figure VI-14. SIMULATED ABUNDANCE OF *Acartia tonsa* AND *A. clausi* WHEN *Mnemiopsis* IS PREDATED AT A DAILY RATE OF 10% (Day 246-365)

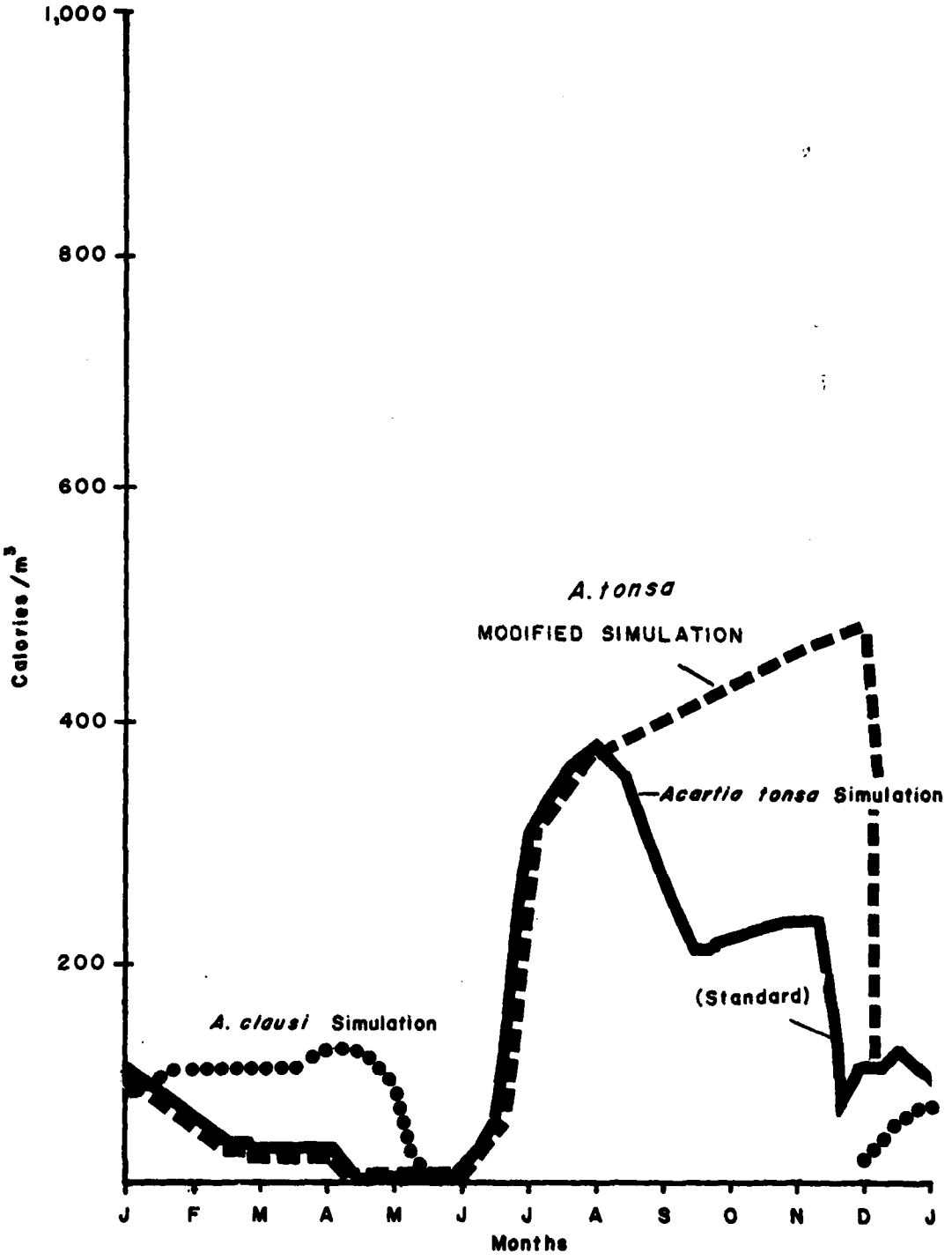

Figure VI-15. SIMULATED ABUNDANCE OF *Acartia tonsa* AND *A. clausi* WHEN *Mnemiopsis* IS PREDATED AT A DAILY RATE OF 20.% (Day 246-365)

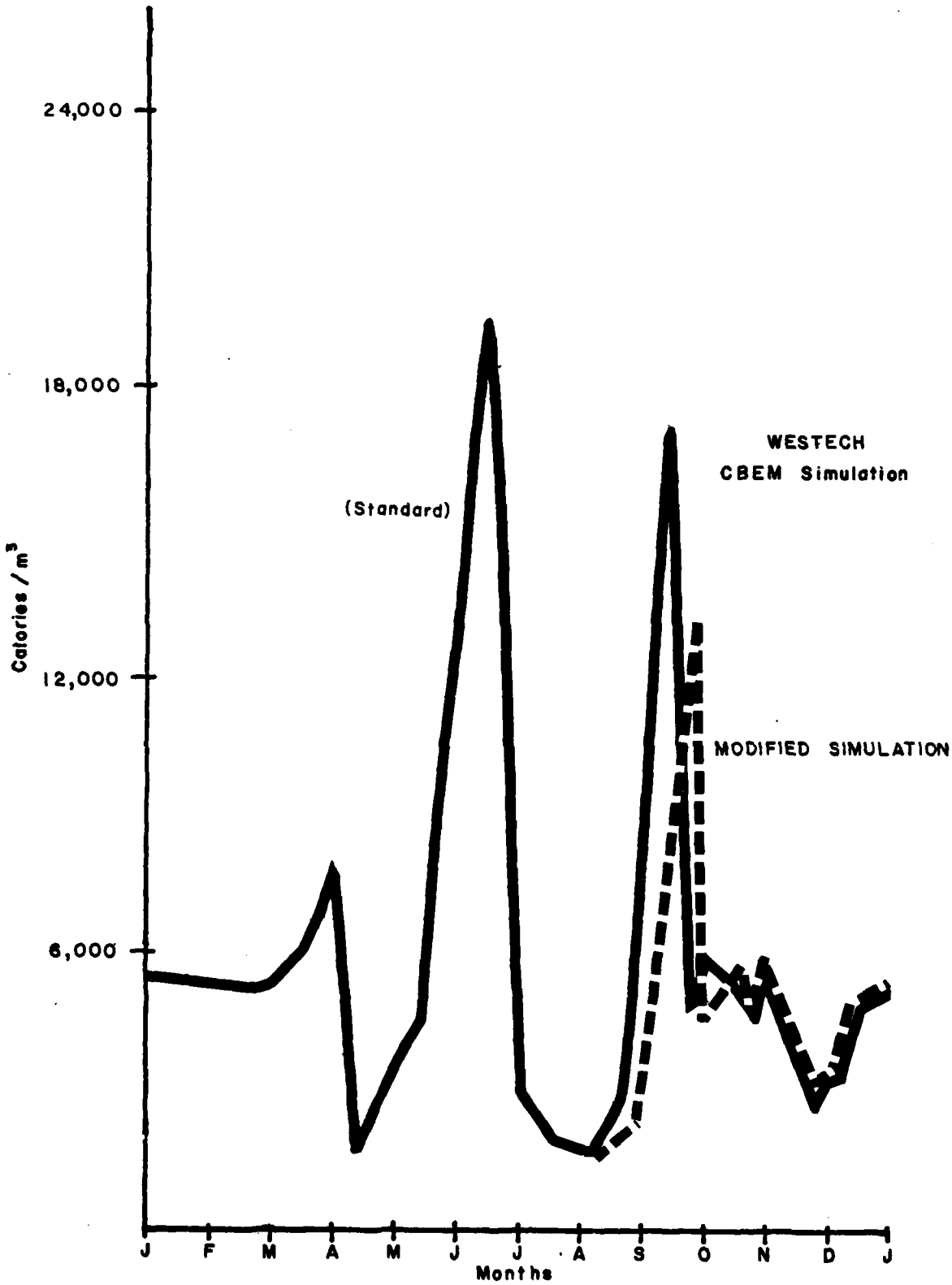

Figure VI- 16. SIMULATED ABUNDANCE OF PHYTOPLANKTON WHEN *Mnemiopsis* IS PREDATED AT A DAILY RATE OF 10%

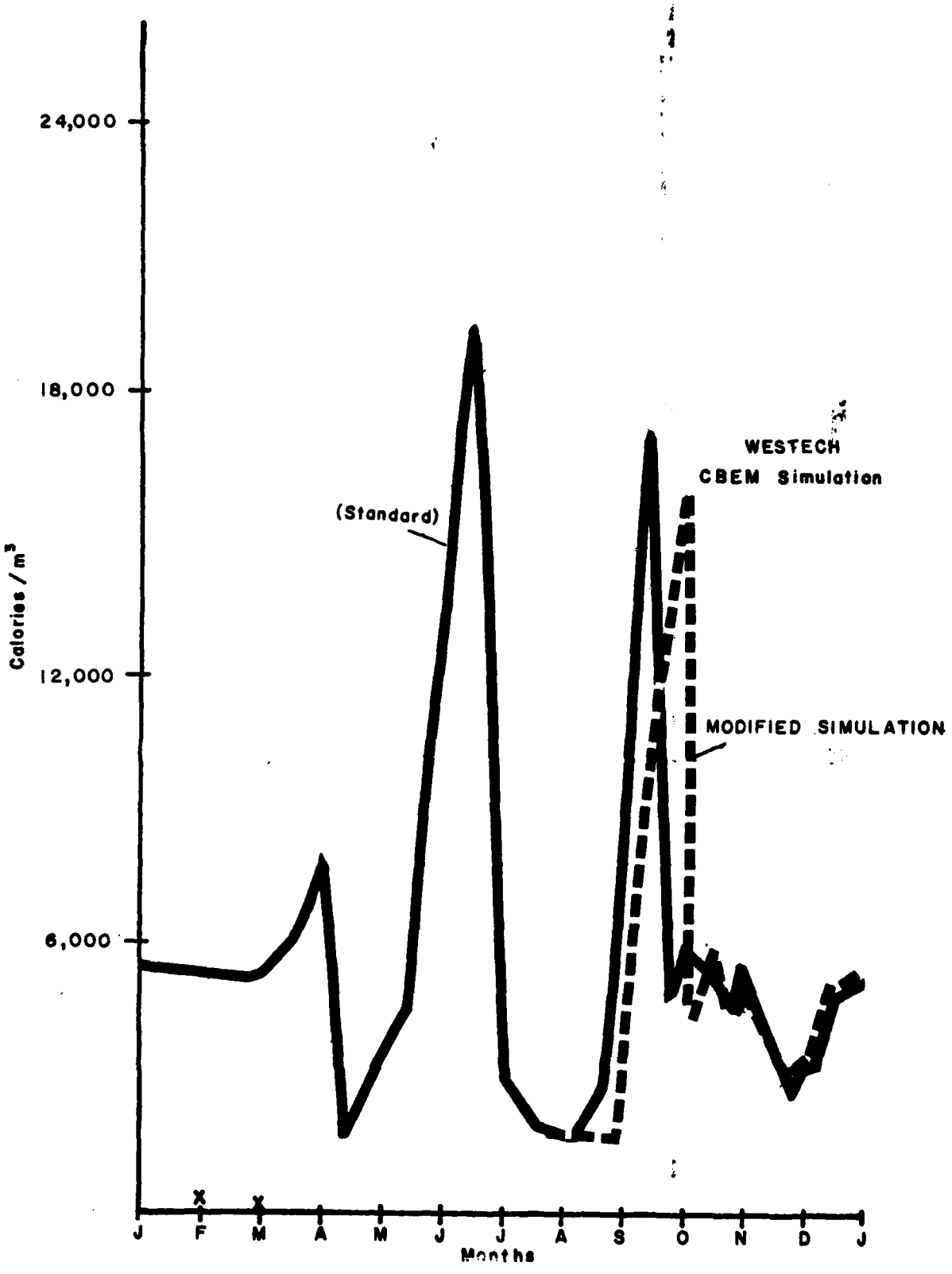

Figure VI-17 SIMULATED ABUNDANCE OF PHYTOPLANKTON WHEN *Mnemiopsis* IS PREDATED AT A DAILY RATE OF 20%

The phytoplankton response to the 50% Mnemiopsis loss (not shown) was very similar to the 20% simulation.

The second preliminary series of simulations modified the physiological response of Acartia clausi to increasing temperatures. A. clausi naupleii were programmed to survive until the temperature exceeded 24°C (the preceeding runs terminated naupleii survival at 20°C (Jeffries 1962). The assimilation to respiration ratio of adults was also altered. In previous runs the A/R ratio was altered to stress A. clausi in an exponential fashion beginning at approximately 13.5°C. In these salinity modification runs the stress did not begin until 20°C.

In this simulation, A. clausi did not begin to decline in late April as previously noted, but increased its biomass several orders of magnitude to a peak biomass in June, after which the temperature-induced stress caused a decline in abundance (Figure VI-18). Although there appears to be only a limited effect on A. tonsa (Figure VI-18), it was enough to cause an increase of about 25% in the spring phytoplankton bloom (Figure VI-19). A. tonsa was apparently kept low enough by competition with A. clausi during the growth stage of the bloom to allow it to grow very large. The small decrease in the fall phytoplankton bloom is probably due to a small number of A. clausi now present because of the modified physiological response. The final effect of this salinity modification run was to increase the abundance of Mnemiopsis earlier in the year, probably as a result of feeding on A. clausi.

E. MODEL USES AND LIMITATIONS

The preliminary altered-salinity simulations discussed above are examples of the way in which CBEM can be used as a tool to aid in understanding ecosystem processes. Specific responses to salinity are being programmed into CBEM whenever the data

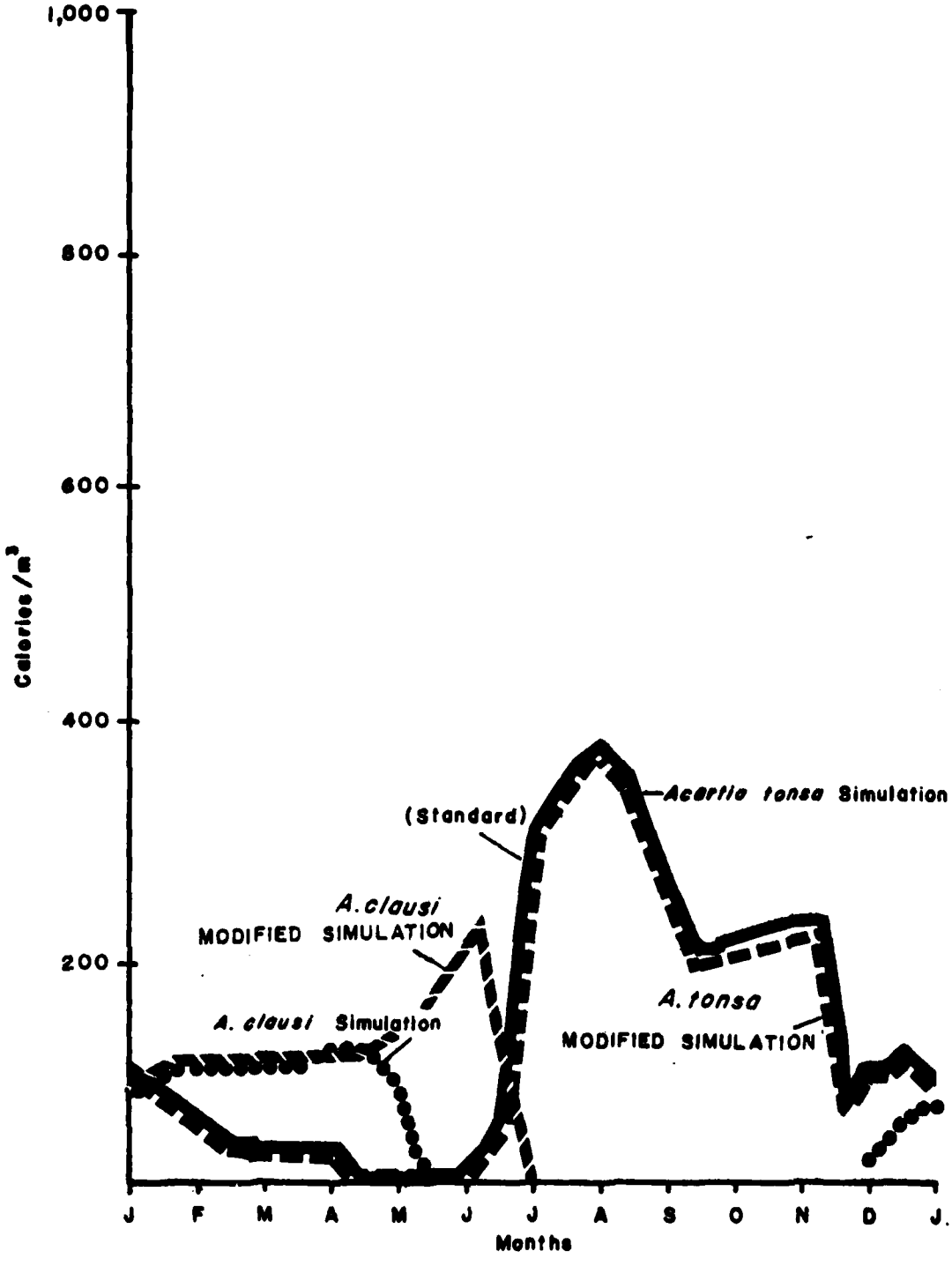

Figure VI- 18 SIMULATED ABUNDANCE OF *Acartia tonsa* AND *A. clausi* WHEN THE PHYSIOLOGICAL RESPONSE OF *A. clausi* IS ALTERED

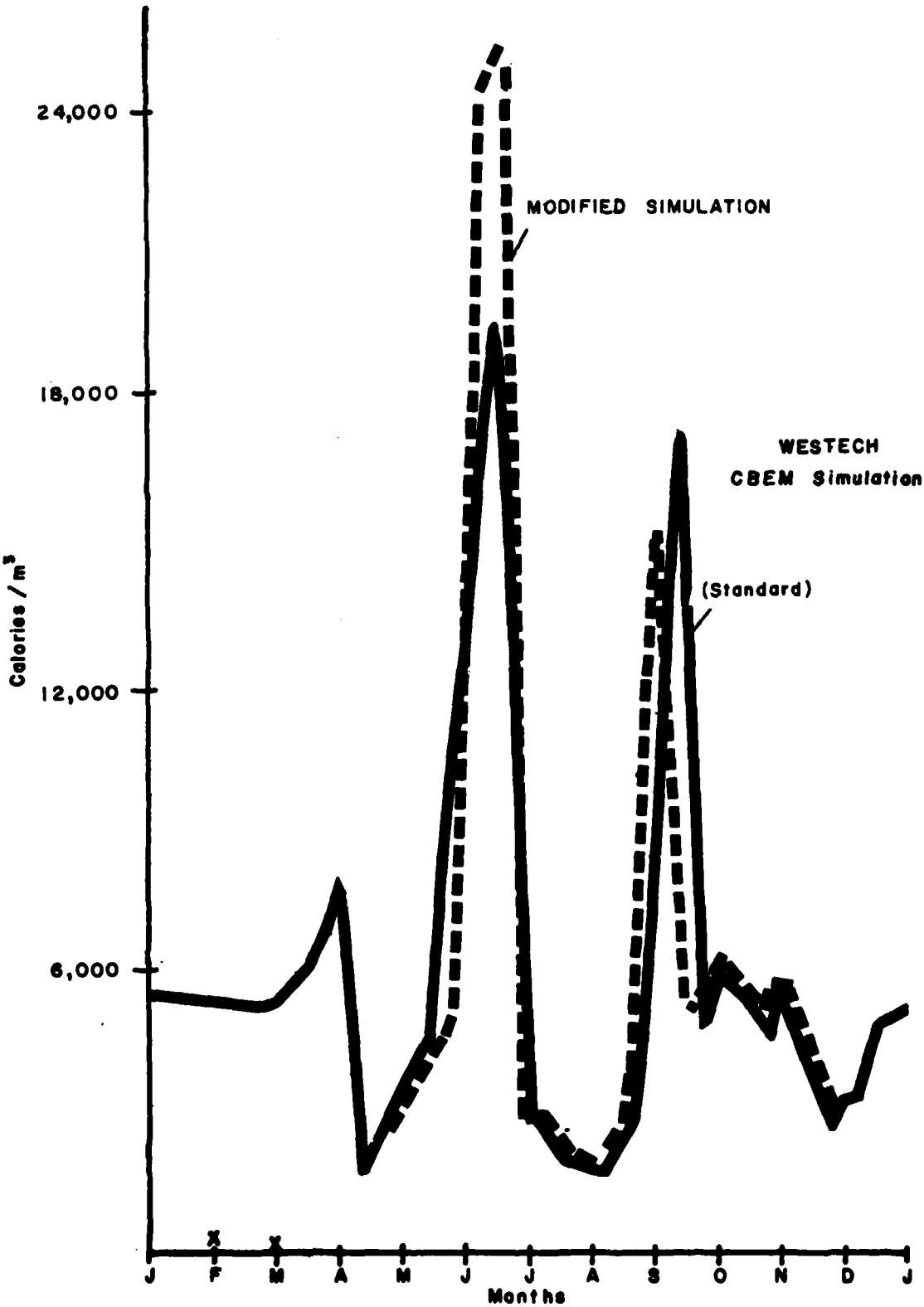

Figure VI-19 SIMULATED ABUNDANCE OF PHYTOPLANKTON WHEN THE PHYSIOLOGICAL RESPONSE OF *Acartia clausi* IS ALTERED

are available. These responses typically include addition or deletion of predators or new food sources, change in respiration, or change in susceptibility to other stresses (i.e. temperature). These changes affect many of the study species depending on specific conditions. When the data are not available, the response must be estimated using the best available information. Either way, the possibilities for combinations of factors are large and a computer is needed to sort out the various results. These results are not exact predictions of behavior of the real ecosystem. They are the end product of feeding a large quantity of information into a computer and asking for results within a highly structured framework. These results can indicate factors and patterns which might be important in the real system. They can also indicate areas where the available data do not seem to explain a simulated occurrence, such as the fall phytoplankton bloom in the CBEM simulation (see above).

CBEM can, within data limitations, be utilized to study salinity-related low flow effects through analysis of alternative salinity scenarios. Given a change of 2-3‰ salinity, for instance, the first task of the CBEM user would be to identify major biological effects (i.e. salinity limitation of predators on food supply, respiration changes, etc.). These effects would then be entered into the CBEM input matrix. Obviously, if the literature defines no known changes, the scenarios will be identical; simulation can predict no more than the state-of-the-art in input data. If, however, differences do exist, CBEM will give the interactive results of a trophic web of organisms acting under the altered salinity conditions for one or more years. This can then be checked and calibrated against known biological behavior insofar as data exists. The power of the simulation is to predict wholeistic interactions of the individual components. In a less direct sense, CBEM can be coupled to other changes (i.e. nutrients) known to change with flow, but only insofar as base data or mathematical calculations allow.

It is clear that without low flow biological data to check against, CBEM results will only be verifiable insofar as they duplicate

"reasonable" biological occurrences. They can, however, be used as a tool to analyze relationships and predict biological response scenarios.

Results of the CBEM can be used then, to predict potential differences in the ecosystem given two or more sets of input variables. Finally, although there are severe difficiencies in the information available concerning the Bay, there is still a great deal of data available from the research that has been done (e.g. Chesapeake Science Vols. 1-18). The goal of the CBEM is to utilize the available data in such a way as to provide insight into the effects of reduced freshwater inflow into the Chesapeake Bay.

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VII. DATA GAPS AND IMPACT ASSESSMENT METHODOLOGY

This chapter is intended to first summarize (Section VII-A) the major areas of missing information or knowledge in the biophysical data base on the Chesapeake Bay. In Section VII-B the summary will be used to develop a rationale for impact assessment methodology which will be used in Phase II of the Biota Assessment. Since the information summarized in Section A has been previously referenced in Chapters III - VI, few reference sources are re-cited here. The reader is referred to the appropriate sections of the earlier chapters.

A. DATA GAPS

1. Physical/Chemical

While the underlying functional principles of Bay circulation have been described, little is known about certain current mechanisms. This lack is particularly severe in terms of quantitative descriptions of currents at depth and their precise modes of interactions with surface currents. The velocity of the longitudinal Bay current which transports many organisms up and down-bay can, at present, only be inferred from the biological data. Its interactions with currents from river mouths, eddy currents or other area specific phenomena are not at all well-known.

In the tributaries, the effects of vertical fronts have just begun to be investigated, although these may strongly affect biota distributions in local situations. Eddy patterns caused by such fronts, or by bottom features or current interaction have only been identified on a few of the better-studied western shore tributaries.

In particular, the relationship between low or high flows and stratification or eddy phenomena has not yet been well documented in a way that permits generalization to other than specific cases. Also, the effects of freshets on the physical charac-

teristics and their relationship to low flow has not been syntheized, and although such information may exist in long-term monitoring records, its compilation would be a major task in itself.

Correlations between flows and nutrients have been carried out on a few river systems; however, the data base does not yet seem strong enough to formulate general rules which hold with any accuracy in most Bay situations. The relationship between other apsects of water quality and flow is generally similar to that of nutrients. It seems, however, that some rough-cut correlations between certain nutrient components and flows can be made, at least for the major rivers. It may then be possible to extrapolate these relations to other, smaller river systems.

The relationship between the "turbidity maximum" and flow is not yet totally clear, although the location of this zone has been charted under differing flow conditions. One of the complications here is the lack of proportional reductions in flows of different river systems under historical drought conditions. Some river reduce flows more than others, and similar patterns are rarely repeated twice in the historical data.

2. Biological

Many of the biological data gaps involve the structure and function of the biotic community itself,while others involve the effects of the physical or chemical system on the biota. It should be noted that the level of detail of information of all types is strongly species dependent, often favoring species of commercial or recreational importance. While this is a logical result, it does pose problems when one tries to assemble a balanced, detailed picture of the ecological system.

Distribution of organisms tends to be well-known in localized areas, usually only for certain species or species groups.

Studies tend to cluster around institutions, areas of water pollution problems, potential power plant sites and other centers of activity or potential environmental problems. For these reasons, some of the smaller rivers, especially those with rural watersheds, have not been well-studied. The Rappahannock and most of the eastern shore rivers are examples of this. In some cases, even physical data such as salinity are only available for these tributaries from scattered time periods.

Dietary information for many of the predators are not well-known. Although stomach content analysis has been performed for certain species of waterfowl or fish in certain locations, variability of diet with location, season, food availability or other factors has seldom been studied, probably due to the complex logistics that such studies would entail. In developing the CBEM (Chapter VI) for example, copepod feeding rates were found to be fairly well-defined, while feeding rates of ctenophores had to be developed mostly from information outside of Chesapeake Bay. Many predators are apparently able to switch food sources fairly easily, while others cannot successfully do so. The question of the abilities of predators to switch could potentially be one of the more important aspects of the actual impact of low flows, or any other stress, on the ecosystem as a whole. Predators with a wide range of potential food sources would be much more resistant to adverse effects than those incapable of switching. There is evidence that some species of waterfowl were able to change diets during the drastic changes in SAV populations that have occurred in the last two decades, although the importance of this "switching" ability has not yet been elucidated.

Biomass data is often unknown or largely unpublished for such major groups as fish. Sampling techniques tend to differ and there are often no obvious ways of standardizing information obtained from different catch techniques. Often sufficient replication of samples is not conducted to assure statistical relia-

bility of any standardization attempt. In other cases, even the methods of measuring biomass (e.g. with or without shell in shellfish) is subject to differing methods of reporting. The seasonality of biomass variations within differing areas of the Bay and the importance of seasonal advances or declines to migration (import - export) data is typically not defined.

Often, entire organism groups have either not been well-studied, or have only begun to be studied. Such groups as nanno-plankton and microzooplankton have only recently begun to receive the attention that they seem to deserve based on their known roles in the ecological system. It is hoped that ongoing studies in these areas will help clarify information on distribution and importance of these organisms.

Standard physiological data such as respiration rates, ingestion andexcretion rates, mortality and natality are often known only in a very abstract sense, even for major species. The functional dependence of these rates on temperature, season, location, presence of predators, or influence of salinity can ofter only be defined in a rough sense or by applying data from areas other than the Chesapeake Bay.

In attempting any synthesis of the data on Chesapeake Bay, one is faced with a patchiness of information, geographically, temporally, and by species. The data were usually taken by a variety of methods and at differing levels of detail. Much basic information has been generated by degree-granting institutions since these bodies are somewhat free of the constraint of having to focus on potential environmental problem areas. Other major contributions have come from largescale, government studies with uniform methodologies (i.e. SAV aerial photographic studies).

The synthesis of this diverse material and its application to impact assessment is of prime importance to federal agencies which have baywide responsibilities. Practical problems such

as the setting of tributary low flows must be met. The available data must therefore be synthesized into a workable methodology for low flow assessment. The conceptual methodologies developed during Phase I for such impact assessment are sketched in the following section. These concepts have been shown during this phase of the Biota Assessment to provide the greatest adaptability to the discrepancies and gaps in the data base, while allowing for the incorporation of new information as Phase II progresses.

B. IMPACT ASSESSMENT METHODOLOGY

The assessment of biological impacts during various low flow scenarios will be accomplished during Phase II of the Chesapeake Bay Low Flow Study. Impact assessment will be based on changes in habitat available to study species under differing salinity scenarios. The salinity data for these scenarios will be provided by the Corps of Engineers based on tests on the Chesapeake Bay Hydraulic Model .

During Phase I, WESTECH is quantifying:

- known habitat
- potential habitat

for 57 major Chesapeake Bay species. Known habitat is defined in two ways depending on the data from which they are derived:

1. If data were obtained from a mapped data set showing actual areas, these areas form known habitat (i.e. SAV maps, see Map Atlas).
2. If the data is derived from studies based on sampling points, we define known habitat as the smallest area meeting basic depth salinity and substrate requirements which contain those points (i.e. benthic maps - see Map Atlas).

Potential habitats are identified by the intersection of data sets which define multidimensional habitats for each organism.

These data sets include salinity, seasonal occurrence within a geographic segment, depth, substrate and requirements for other organisms as outlined in Chapters IV and V. Total potential habitat area includes both known habitat and other potential habitat areas.

Many maps in the Map Atlas show known and potential habitat combined due to geographical data gaps in distribution information. However, in all cases possible,known habitat area is mapped by organism. In some cases this is broken down by organism lifestage or seasonality.

During Phase II, potential habitat areas of study species will be mapped under salinity scenarios for an average Water year, for the 1960 drought, and consumptive water use (year 2020). The basis for this mapping will be the same habitat criteria developed in Phase I; depth, salinity, seasonality, substrate and presence of other required organisms. The degree of impact will be quantified by a comparison between habitat under average inflow conditions (modal hydrograph) and habitat available to the organism under each scenario.

There are several possible cases which will determine the methods of comparison to be used:

1. If known habitat is poorly defined under base conditions, or
2. If known habitat is essentially identical with potential habitat under base conditions, impact will be a ratio defined as the quotient of potential habitats under future scenario and under base conditions.

$$\text{Impacts} = \frac{\text{potential habitat (salinity scenario - X)}}{\text{potential habitat (base conditions)}}$$

3. If known habitat has been well defined on a consistent basis, it is reasonable to assume that the species distribution may not completely fill the potential habitat.

(The reasons for this discrepancy include the fact that we have not completely defined all habitat

variables, as well as the fact that dispersal mechanisms and colonization rates affect the geographical distribution of a species.) In this case, we will assume that the percentage of potential habitat occupied will remain the same under base and and future conditions. The amount of the species existing under a particular salinity scenario will be defined by:

$$\frac{\text{potential habitat (base conditions)}}{\text{known (realized) habitat (base conditions)}} = \frac{\text{potential habitat (scenario-X)}}{\text{projected realized habitat (scenario-X)}}$$

where in addition to projecting potential habitat through use of the ratio defined for points 1 and 2 above, a projection of the currently realized habitat can be made for appropriate species. This may prove particularly useful for species such as emergent vegetation where the coverage of known habitat is well known from aerial surveys.

With any of these projections, it is important to realize that there is a considerable margin for error in such prediction. this margin or error is due to the fact that the impacts will be dynamic and will evolve with time. Colonization or dispersal effects are not taken into consideration. Also, other habitat variables have not been taken into account by the methodology due to complexity of including other variables and the lack of good data.

In Phase II, known and ptoential habitat will be measured on an individual species basis for each low flow scenario for each of the 13 geographical subdivisions so that each geographical area can be handled as a unit (see Figure VI-1). In the analysis of salinity scenarios, species may, of course, transfer their range from one compartment ot another, or ranges may expand or contract. Where possible, impact ratios will be calculated for each compartment as well as being aggregated for the whole Bay.

Also, factors which may <u>currently</u> preclude a species movement to another area - even one which it may have occupied during the past - will be addressed, where known. For example, the dramatic change in SAV distributions in recent years may be partially due to increased runoff of toxics (including herbicides)

in rivers which drain urbanized portions of Maryland and Virginia (EPA studies in progress).

As mentioned, these impact ratios are based on imcomplete data about organisms. Colonization, species dispersal rates and other factors contribute to differential use of potential habitat areas within a species. One cannot, at this time define all habitat parameters or make completely accurate correlations even with identifiable parameters such as substrate. Thus the impact ratios may be subject to considerable error margins.

As an example of the impact assessment procedure, consider species "A" which is a marine-type species and species "B" which prefers polyhaline salinities, but can withstand marine salinities. Consider alos that A preys upon B. The impact assessment procedure will then consist of several steps. First the habitats of both A and B will be mapped under "average inflow" conditions from hydraulic model data. Secondly, the species distributions will be mapped under one of several salinity scenarios (for our purposes here, we will use the 1960's drought). Thirdly, the difference in habitat areas will be measured. This constitutes the impact ratios discussed in this section. Lastly, the conceptual or mathematical (CBEM) models will be applied to determine the effects of species interaction as time evolves. This information will be used to modify the interpretation of the impact ratios, which in themselves, represent only instantaneous, direct effects and take no account of trophic interactions.

To reduce the possibility of readers using these ratios as highly accurate impact predictors, they will be used only to define broad categories of effects. We have not at this time finalized a category scheme, nor is it appropriate to do so until the types and magnitudes or errors inherent in the ratios can be estimated based on comparisons with historical data or other means (i.e. 1960's drought). Attempts at calibration will be made using those organisms for which drought data exists (only available for a few organisms) and through use of the conceptual and CBEM models. This is expected to generate an impact classification similar to the example below for the Impact Ratio (IR) for potential habitats.

TABLE VII-1. Example of Possible Primary Impact Classification Scheme.

$$IR = \frac{\text{(salinity scenario - X)}}{\text{(base conditions)}} \text{ potential habitat}$$

Range - IR	Classification
0 - 0.7	Severe nagative impact
0.7 - 0.9	Moderate negative impact
0.9 - 1.1	Low impact
1.1 - 1.4	Moderate increase or enhancement
1.4 +	Severe increase or enhancement

It should be noted here that if a species shows an immediate positive effect, a net gain for the ecosystem is not necessarily indicated. This effect may be short-lived in time or canceled by net drops in population of other organisms due to shifts in the Bay's trophic systems. We will attempt, to the extent possible, to analyze the changes in direct impact of each species on overall ecosystem function based on known interactions from the base period. Such analysis can only be based on conceptual or mathematical models of ecosystem function.

The use of some trophic model is necessary in order to meet the objectives of both Corps and Legislative decision-making which may result from the low flow study and other portions of the Chesapeake Bay study. The use of impact ratios outlined above gives a response considering each organisms as an isolated entity. In fact, organisms are linked to each other through feeding, competition, predation and other biological relationships.

The eventual equilibrium state of the ecosystem following a drought or after an extended period of lower flows will depend strongly on these interactions. For instance, if impact ratios of oyster predators show increase of biomass (or habitat) in one area of the Bay, oyster biomass can be expected to eventually decrease in these same areas due to the extended predator penetration. Such effects can only be ascertained by examining potential habitat overlaps between species which affect each other, either through making judgements based on the conceptual relationships, or through modeling the effects of the increase in both species as a predator-prey relationship over time with a mathematical model.

Due to lack of data, some such instances must be addressed at a conceptual model level only. To accomplish this, the conceptual model developed in Phase I and supporting compartment models will be used (see Chapter VI). In cases where the data are adequate to define basic species parameters and physical

driving functions, it will be possible to apply the CBEM mathematical model. Such modeling can be used to identify not only gross probable outcomes (impacts) but may in some cases indicate the time evolution of the system following the impositions of drought conditions. Even in cases where precise quantitative analysis of stress effects on the ecosystem are not possbile, the mathematical model can be used to illustrate the distribution of that stress on ecosystem components by means of sensitivity analysis (which entails measurement only of percentage changes compared to the change in a particular stressed parameter; see Patten 1971).

VIII. CONCLUSIONS

The object of Phase I of the Biota Assessment has been to synthesize and standardize existing data and studies on Chesapeake Bay and develop methodologies to serve as a basis for low flow impact Assessment. The existing literature, published and unpublished , is present in a diversity of forms. Large amounts of information on physical, chemical and biological aspects of the estuarine system have been collected over the past 2 to 3 decades. However, each study is designed to meet its own particular objective, resulting in differing study methods and reporting formats. Although several person-years have been spent in Phase I of the Biota Assessment, we have merely scratched the surface of synthesizing and standardizing some of this information, limiting the study to major information concerned with certain "study species".

Knowledge of the physical dynamics of the Bay is based on many detailed monitoring and theoretical studies by researchers from government and academic institutions. There are still major unanswered questions about overall Bay circulation, and large inconsistancies in the understanding of tributaries and local effects of altered flow regimes. Although the Environmental Protection Agency and others have been devoting considerable effort to understanding this system, physical dynamics are complex to monitor or model and the present state-of-the-art does not permit accurate quantification, particularly of many subsurface phenomena involving circulation.

The chemical and nutrient cycles are in a somewhat similar situation. Here, though, some progress has been made with the major nutrients, and budget analysis has been carried out on some of the major tributaries. Some efforts have even been made to relate nutrient levels to flow, although such studies are still in early stages.

The biological systems of Chesapeake Bay are of similar complexity. Here, however, we have been able to reproduce major aspects of structure and function of the estuarine community through analysis of the literature, habitat classification and limitation to major species, followed by conceptual and mathematical modeling. It has been found that major trophic responses can be reproduced for purposes of investigation of salinity stress on Bay organisms.

The Bay literature is voluminous. Many Bay organisms have been heavily studied; however, others are known only from taxonomic collections, not ecological or distributional research. A series of trophically oriented ecological studies of various Bay areas with consistant methodologies would be the only rapid method for closing many of the data gaps that exist. For certain organisms it is possible to define habitat; however, this is limited to a few major variables (i.e. depth, salinity, substrate, etc.). Even for these variablesthere are some inconsistancies in measurement techniques. More subtle effects and variables such as dissolved oxygen, nutrients, etc. have been studied only in isolated cases. From those organisms which have a data base encompassing distribution, seasonality and ecological function, we have mapped distributions of 57 "study species" during a "base year" which represents average flow and (presumably) salinity data.

It has been possible, based on assimilation and synthesis of major Bay-related literature, to develop detailed conceptual models of functional ecological units (compartments) and synthesize these into a broad conceptual model which represents major pathways of Bay energy flow. From this conceptual model, it has been possible to select and test a mathematical submodel on one of thirteen geographical Bay units (segments). This submodel is in good agreement with published data for this area. The computerized mathematical model (CBEM) is stable but dynamic. It is sensitive to salinity variation and should pro-

vide a powerful tool for future work on ecosystem stress.

Many data gaps exist with respect to organism distribution, stress tolerance , ecological functions, etc. However, enough of this information exists to construct a good first-cut at impact analysis of flow differences using tools developed in this phase of the Biota Assessment.

The first step in such impact assessment will be to map habitats for study species under "normal" and various low flow conditions to identify species reactions. These reactions are only immediate, primary reactions to the stresses imposed by low flow conditions. With the passing of time, trophic effects, dispersal, colonization, competition and seasonal factors all come into play. While conceptual models can be used to analyze and predict these effects to some extent, mathematical-computer models such as CBEM add power and extend the capabilities of such analysis. CBEM can be used to analyze either short-term, immediate reaction to stress (sensitivity analysis) or track the system over time. In order to accomplish this, adjustments for the physical and chemical characteristics of each tributary or Bay segment must be made. The model has been shown to serve as an effective tool to analyze effects of trophic interactions and is in agreement with existing dynamics on the estuary tested (Patuxent).

The purpose of Phase I of the Biota Assessment has been to develop tools and methodologies for analysis of hydraulic model data in Phase II. Both the tools and the impacts assessment methods have been developed and (at least theoretically) shown to be effective and workable. During Phase II of the Biota Assessment the tools will be applied to scenarios involving differing flow and salinity regimes as a part of the Corps of Engineers overall Low Flow Project for the Chesapeake Bay.

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